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<p>(51) International Patent Classification 6 : <b>C12Q 1/68</b></p>	<p><b>A2</b></p>	<p>(11) International Publication Number: <b>WO 98/20165</b></p>
		<p>(43) International Publication Date: 14 May 1998 (14.05.98)</p>
<p>(21) International Application Number: PCT/US97/20313</p> <p>(22) International Filing Date: 5 November 1997 (05.11.97)</p> <p>(30) Priority Data: 60/030,455 6 November 1996 (06.11.96) US</p> <p>(71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Massachusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).</p> <p>(74) Agents: GRANAHAH, Patricia et al.; Hamilton, Brook, Smith &amp; Reynolds, Two Militia Drive, Lexington, MA 02173 (US).</p>		<p>(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).</p> <p><b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i></p>
<p>(54) Title: BIALLELIC MARKERS</p> <p>(57) Abstract</p> <p>The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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-1-

## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

-2-

RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater



-3-

frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a  
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays  
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for  
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to  
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

- 4 -

## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

- 5 -

## DETAILED DESCRIPTION OF THE INVENTION

## DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

-6-

polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

-7-

and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

15 A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

20 Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

- 8 -

conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

- 9 -

and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

-10-

samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For  
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.  
10  
15

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),  
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification  
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

### 30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,



-11-

sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 20 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

-12-

hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

-13-

sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of  
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30 1988)).

-14-

## 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

## 10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

## 25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

-15-

## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

-16-

match of suspect and crime scene sample would occur by chance.

$p(ID)$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

10 Homozygote:  $p(AA) = x^2$   
 Homozygote:  $p(BB) = y^2 = (1-x)^2$   
 Single Heterozygote:  $p(AB) = p(BA) = xy = x(1-x)$   
 Both Heterozygotes:  $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

15  $p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2$ .

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(ID)$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

25  $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(ID)$  and  $p(exc)$ .

The cumulative probability of identity ( $cum p(ID)$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30

$cum p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$

-17-

The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

- The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.
- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25        attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- The probability of parentage exclusion (representing
- 30        the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

-18-

incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the



-19-

circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

-20-

(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

-21-

might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

-22-

D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

-23-

for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of

10 obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ),

20 ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

- 24 -

Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate  
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod  
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.  
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some  
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)  
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

-25-

corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or  
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate  
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host  
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include  
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as  
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing  
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

-26-

The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate



-27-

the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

-28-

100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

#### 15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

-29-

comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

-30-

corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

-31-

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	C	T	---	---	TGTGAACCTCCACTTGAAGCCAAAGAAAGAACTCACACCTAAAACACATGCCAGTTGGGAAGGCTGTGAAAACCTCAGTGCATATAGGAACACTTGAGACTAATGAAAGAGAGAGTGGAGACCAATCTTTATTTGTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATGGAAAAAGCTTTGAGGATAATGTTACTAGACTTTATGCCATGGTGTCTTTC/TAAGTTAATGCTGTGCTCIGTCAG
WI-10744	61	G	C	---	---	AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC[G/C]AA AACACTCTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTTGATAATACATAAGCCCCCTAGGATTTAGATACAACTCTTGAAGAAACTGAGACAGATAATCTGAATTAATGAGGTAAAGTTTCAGGCACCTCA
WI-9975	126	C	T	---	---	GGGCAAAATTACCAGCAAAAAGTCAAAITACCAGCATCAAAGTCAGGTGCAAGGAGGTAGAACAATTACAGTAACATATGCAATCTTTTGTTATATAGTATATCTGCCCAATGCCCTAGAATA[C/T]AGTGGTCCCTAATAGTATTAGTCCCTTTTCTCCTCTCTCTCACTCTCTGAAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAAATGTGTATATCAATTTGATTTCTACTGAA
WI-8010	247	G	T	---	---	GCTAGGTTTTGTTCTGTTGGCTGCTTCACTAGACTTGAGATGACTTGAATTTACAGTAATCCCTATGTTGATGTAACCTAGCTAGACCTTCCCTCTCCGCAATCCCAGCTCCAGGTTTCAGAAAGTATGCCACAC TCACCCCTCTCTCCAGTTTCATCTGTATTAATTTCTTCCCATATTAATTCAAAGGGAGTGGACAGGTCCCTGGCTGAAAAGAAATAAGAGATCCCCAAAGTGGTGGGG[G/T]CTT
WI-5222b	85	G	C	---	---	GCOCGGCTATCTTTTAATTTAACTGTATCTTTGGTGTCTTCCATCCTAGGATTTGCTGCTTATAATCTTTGCTCCTGTGTA[G/C]ATACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGTAGTAGTGCCAAITCTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTATCTGGACTCTATAACAACCTCCAACAGAA
WI-5222	52	G	C	---	---	GCCCGGCTATCTTTTAATTTAACTGTATCTTTGGTGTCTTCCATCCTCATCCTA[G/C]GATTCTGCCTTAT AATCTTTGCTGCTGTGTAGATTACCTGATTCATCTTTTGATACACAAGGCTGATGGCTCACAATGTAGTAGTGCCAAITCTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTATCTCGACTCTATAACAACCTCCAACAGAA
WI-8007	242	C	A	---	---	TATGCACCTCCACAAAAGCGATATAATTTAAAGTTTTTTTTCATTAGAAATAAATGTATAAAAATAA ATATGTTATTATAGGCATTTATTACTAACTATAGTCCCTCTTGGAAAGAACACCCAAACCAATACTTATAAAGTACATGTAATTTATAGTAACATATTTTACTATATACATATGGAAGAAATCATATTTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAC[C/A]AGCTGCTG
WI-9823	97	C	T	---	---	TCAGTTGCAAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTGTTTGTAGTCTATATTCACACATATGAGTGAAATTTTC/TTGGGGCATGGGAAATACATCTTTATGAGACATTTGA ACTGCTCACCACCTATCATAGTATCCATTTAAACAGACCAACAAATGTATAAGAAATCCCTTTGTTTTCATGCTTTCCCAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	TCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGGAATCCTTTCTCT ACTTGCTCCTCATGTACAATTTTCTGCTCGTCTTCAJATJGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCTTATAGGCTCTG TCTTAAACCTGTAATGGTATATTAATCCCTGGTGTGGAATGCTCTC
WI-9651	139 T C ---	---	TCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGGAATCCTTTCTCT ACTTGCTCCTCATGTACAATTTTCTGCTCGTCTTCAAGGGCAGCTTGCAAGCCTCCCTTTAGACACCT CTJACAGGTACAGCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCTTATAGGCTCTGT CTTAAACCTGTAATGGTATATTAATCCCTGGTGTGGAATGCTCTC
WI-7676b	309 A C ---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGCTGCTGGGACTTGGCCCTGCTATTTTGTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTCTCTGGTGGCTGCTGGGTTCAGGGGCAGGAAGCGTGTGACTGCAGCTTCTGCTGTGTC TCCCCCGTCTCTGGAGGCGATATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGCTGCTGGGACTTGGCCCTGCTATTTTGTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCJTGCGCTCTCTGGTGGCTGCTGGGTTCAGGGGCAGGAAGCGTGTGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCTGGAGGCGATATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGCTCTGGTCTGTTCAATCACTTCTCTCTCCAAATGAAGGATATTTAAGCATCAAT CATCTGGCCCTTTTGTGAGTTTGAATAATTTTGTGJATGACTCCTATGCACATGATAAATTTGTTA TGTCTGCTCTTATCTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAGGA TCACCCCTTTTGGCTCTACAACTTATAGATAATTTAATATCTTT
WI-9986	42 T C ---	---	TTGGTGAACCTCAGAAATATAGGAAAATAGACAAATTTGAAT/A, C]GTACCCCGAGGAAACAAGAG CCCTGCACTTGACTCCAAAGGAGTCTATTTCTGGCTGTTCCAGACTTTATGTATCTTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGTAGTACTCACAAGAACAATGTCA ATATCAATAGCATGCATATGGGTGTTGGATTCTTAGAACTTATTGCAAT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATCAGGCCAAGTGGAGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCCCTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTATTT CAGGGCTTGCATGGCTCTATCCCTCTGCCCTCTC]ACCACCTTCTTTGGAGCAAGGAGATGC AGCTGATTGTGTAAACAGCTCAATTTGTACAGTGTCTGTATGTAATAA
WI-7224	134 T C ---	---	ATAACCCCTTGTGATGTATCAACCACTCACTAATTTATCACTTATGTGCTATCAGATATCCTCTCT ACCTCAGCTTATTTTGAAGAAAATCCTAAACATCAAACTTTCATCCATAAAAAATGTCAGCATTT /CIATTAACCAATAAATCTTTTAAAGAAAACATAAGGACACATTTTCAAAATTAATAAAAAATAAG GCATTTAAGGATGGCTGTGATTATCTTGGGAAGCAGAGTATTCATGCTAG

WI-10826	132	A C ---	---	TCATTATTCACAGTAGCCCATGAAGTAGGTATAACAGCCTCTATTTTAAATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCTTAATAAGCAAAGACCTGCAJ/C JCCCTGGCTTCCTGACTCCAAAGCTATCCCTTCTCATGCTGTGCTCAGCCAGGACCCCATGCGCA GAAAGCCCGAGCCTCTCCATCCCCCAG
TIGR- A004S25	145	G A ---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACTTTGGAGATTCAITTTCTTGAGTGGCAGCTGCAT GCTCATTCAGTGAAGAACTTTGGGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACCTGCTTAGGCATTGAACCATCACCTGGTTTGCATTCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24	A T --	---	AAACACAGAAATCATCAAAGCACJATJATCTGTGTTTGAGATAATGATAGTCTGAGTCACTTAIG TAAGAAGTAACTCTGAATAGTAGGATAGTATTATCAITTCCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAACCTCTCCGTACTGTAAITTTTCAITTCATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	G T ---	---	TAGTATGTCACTGCCATGGTAAGGACTTTTGATCACTAGGAAATAAGAACACTTTGAATGGCTTGCC TTTCAATAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCATT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAAAGAGATTAAAGAAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107	T G ---	---	TTCAITTCCTTCCAAATCCTTAGGAAATTTACATTATGGCTAGTGTCTTTGGGTGTGAGCGGATT ATGCTGAGGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATTCGTCTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACITGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-4719	70	G A ---	---	TTCAITTCCTTCCAAATCCTTAGGAAATTTACATTATGGCTAGTGTCTTTGGGTGTGAGCGGATT AT[G/A]TCTGAGGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATTCGTCTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACITGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-9484b	216	G C ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGGAAGATTCTTACCTTACCCCTGAGG AATACTGAGTCCGATGCAGGGGAATGGGTGGGGTGTTACCACCTTCTCTGACACACTGCCAAGT TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGGCCAGACAGGGAATTCAGGGCATGTATGGCTC AGTCCACCTCT[G/C]ACTGCAGAGTATAGGGACCAGGGTTCCAACTTT
WI-9484	178	G A ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGGAAGATTCTTACCTTACCCCTGAGG AATACTGAGTCCGATGCAGGGGAATGGGTGGGGTGTTACCACCTTCTCTGACACACTGCCAAGT TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGGCCAGACAGG[G/A]JAGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAACTTT



WI-7330	207 C T	---	---	AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTGCTT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTTAAATTTGGCATATAGGTTT GTGACACAGAAGTCTACTTTGGTGGCTAAGTTTCTACTAAGGAAAAAATACTGAAAGATTAAAAAG TGAGAGTC/TJTGAAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTACAG
WI-9443	211 GA	---	---	TTAAAACAGTTCAGTTGGTGAAGCAGAAAGGATGTGATTACAATTTAAATGAATCAGTCACCTT GCACAAATTAATCCTCTTGGCATCATACAAACTGGGTTTAAATGGCAAATGATGACATCATAGCATGA CCAACTCATGGAAGGAGTCTAGAGTCATCAGCTCAGACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC/GA/CAGAGACCTTGGACTACAGATGACACCACATGCCACCTT
WI-7166	59 CT	---	---	TCTCTCAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA/C/TJGGAT CATCAACAAGATTCCTTGTGCAAAATATTTGACTATTTCTGATCTTTCATCTCTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGGTTTAACTTTGCTGTGAACAATTTGCGAAAAAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCGAG
WI-7259b	189 T C	---	---	GCCTTCTCCACGGAAGCGGGTCTTGGCCTGGAACTTCCAGAGAGGAGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTCTTCTCTCTCTGAGTTCTCTGGGCT GGCAGGCTCCCTCGGAAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAGT/C/TJGGGGGAGCAG AGCAGCAGGTGGACAGGTGTTTCAGGGGGCCCAACTTCCCTGGAGCTC
WI-7259	188 GT	---	---	GCCTTCTCCACGGAAGCGGGTCTTGGCCTGGAACTTCCAGAGAGGAGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTCTTCTCTCTGAGTTCTCTGGGCT GGCAGGCTCCCTCGGAAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAGT/C/TJGGGGGAGCAG GAGCCAGCAGGTGGACAGGTGTTTCAGGGGGCCCAACTTCCCTGGAGC
WI-7322	275 AG	---	---	GTACTTTAGGCTGTGGAGGTGGCATTAGTGGTGACCTTGCACAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG GCCATAAACTGCCTAAGCACTCAGGCCCTCCACTCATCAACCCCTTGACCAGAGAAAGAAGCACTC TGGTTCTATCCCTTGTACATAGAGAGTTTGTATGGGGCCCTCTGGCTG
WI-7685	46 T C	---	---	TCAGTTCTAGTCTCTGGGGCCACAGAAACTCTTTTGGGCTC/TJCTTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGAGCCAGGTCTTGGAGCTGAGCCCTCACCTGTACTCTTCGAAAAATCTCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCTCTCTCTCTCGCGACTC CTGGTTGAGCTGTGGCTCAGTCCCAACAGATGCTTTTCTGTCTC
WI-563	87 GA	---	---	TGTGACCAATTGTTATTTAGAGGGTTTAAATGGCCTGACTATACCTGATGGTGGCCAGAATTTC CTGGGGAGGGCTCCCTT/GA/CCTGATGATGCTACCTAACTGCCTACTCTTAACAATACTACTCC TGTGTTATGGGGATCCTAAGCCAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCCAAATTTAAATCTCTTTGGATAACCCAGGGACAT

WI-931c	191	C A ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCACAAATGATCCTTCT GTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCC[C/A]GAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGTCAGA
WI-931b	81	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACACCCCTGGAGTT TCTCTCCCTCCCT[AG/TT]CCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCACAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGTCAGA
WI-931	31	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCAC[AG/GCC]ACTAGCCCTGAACCTTGACACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCACAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGTCAGA
WI-10870b	91	C T ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGG[C/TT]ACCTACTTAGAGAGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCCTGATACAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAAGTTGCCCCCCC
WI-10870	103	G A ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGGACCTACTTAGAG[AG/AC]AGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCCTGATACAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAAGTTGCCCCCCC
WI-7719b	281	T C ---	---	AGTTTATCTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTTATCTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[AG/TT]TAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCCTCCACTTTTCATTTTCTTGAACATTGCTATCAACTGGAA GAGT[C/AG]GTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTCTTTCTTTTGTGA TGCCATTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---	---	---	TCCCTTTATGACCCCAAGAGATAATTTATTAAACACCAATTACGTAGCAGGCCATGGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGGCG/GTCCAGGTGGAACTATGCAGTGTGCTCCGGCCACACA TCCTGCTGGGCCCCCTACCCCTGCCCAATTCATCTCTGCCAATAATCTCTGCTATTGTTGTTTCATCCTG GAGATTGAAGGGAGGTCAAGTGTGTTGTCAATGATTGTGCAGAGAACCT
WI-7842	57 T C ---	---	---	CACAGCCATGCCCTTGAGGAGCGCGGCCACCCAGATGCTGAATCCCTATCCCATCTCTG/TG/TGATGAG TCCCATTTGCCCTTGCAATTAGCATTCGTCTCCGCCCAAAAAAGAAATGTGCTATGAAGCTTTCTTTCCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTTCAGCTGCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAAATGATTGAGCTCCCTTATA
WI-7721	145 A C ---	---	---	CTGCCTCATACGCCCACTGGAGTCCACACTTGAATTTGGGAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGGCCACATCCCAACCCAGCTGTACCCAGCCCGGAGGTGCAGCCCTTCCTCCOC TGTCTCTGC/A/C/JTCTGACTCTCTTTTGGGTCCTCTGTATGCTACCTCTGACTTCTGTGTCCTCTCTG TGTCTGCTCTCATCTCTCTTACTGGGCTGGGGCTAGCCCAA
WI-4767b	173 C A ---	---	---	TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCT CAGGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTGGAGAGGGTATGTTT CTTGCCTTGAGAAATCCTAGAAAGCACACAGGGATGACA/C/A/JAATCACTAAGGAAATTCCTACTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G ---	---	---	TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCT CCTCAGGTCTGGTAACTCTAGATCTTCTATATCCATTGAGTGTGATGGAGTGGAGAGGGGTATG TTTCTTGCCTTGAGAAATCCTAGAAAGCACACAGGGATGACACAAATCACTAAGGAAATTCCTACTAAGAC TCTCTAACCCAGAGATTTTAACT
WI-7718f	222 C T ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA/C/T/CATGCAGGAAGGAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT/CJGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31 G A ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91 C G ---	---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAACTGTTGTTGAAACAGAAAAATAAGTGC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248 A G ---	---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAGT ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAACTGTTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[A/G]AT
WI-7718a	42 A T ---	C	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGC[A/C]TGTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAACTGTTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[A
WI-7227d	99 G C ---	---	---	AGGGAATTGTTGTTGCTCCTGGAGGAAGCCCCAGGCATCATTAAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTTCATCTTTTCAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---	---	---	AGGGAATTGTTGTTGCTCCTGGAGGAAGCCCCAGGCATCATTAAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTTCATCTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227b	93 G T ---	---	---	AGGGAATTGTTGTTGCTCCTGGAGGAAGCCCCAGGCATCATTAAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTTCATCTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	---	AGGGAATTGTTGTTGCTCCTGGAGGAAGCCCCAGGCATCATTAAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTTCATCTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---	---	---	CCCAATGCCTCTCCACGATGTCAAGGACTCCTGCTGCTCCTGGAGTGGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGCTACTGCTATGTTGTGATCCTTCATCGAACAACACTGATCGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAATGAGCCAAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[NC]ATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	---	CCACAATGCTCTCCACGATGTCAGGACTCCTGTCTGTCTCTGGAGGTGGGAGACAAGGAACCTT/A JCCGAAGAGGAAGCAAGAACCGTACTGTCTATGTGTGATCCTTCATCGAACAACTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACGTAGCCAAACACACTGT AAATATCCACAGACTCCTCCCTGCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCTTTGACCTGCCCTGGACTCCTATGATGGCTGTGTTGATATAATCA GATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAATGGGTCC CTGAGGAGAAATCTGGGAGGAGCTG/G/GTGTGATGAAGGTGATGTTGGGAGGGAGCACAGTGT CTGTGGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCTTTGACCTGCCCTGGACTCCTATGATGGCTGTGTTGATATAATCA TCAGATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAATGTC GTCCCTGAGGAGAAATCTGGGAGGAGCTGATGATGAAGGTGATGTTGGGAGGGAGCACAGTGT TCTGTGGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTCTTCTTCTTCT AGCCCTGCAAGTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAGATC AGATGTGGCCCAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAACGGCTCTGTTGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTCTTCTTCTTCT ACCAAGCCCTGCAAGTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAG ATCAGATGTGGCCCAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCTCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTCTTCTTCTTCT ACCAAGCCCTGCAAGTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAG ATCAGATGTGGCCCAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCTCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATTGCTCTATTGGACCTCATATTAAATAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAAGAG/G/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGCTCTTCCCATTTTACAAATAGGAGACAAATAATAGGAGATTAAATAACTCATCAC TGTTTTCAAATAAGGAGTGTGAGGTTTGTGCC
WI-1017a	92 G A ---	---	---	AAATTGCTCTATTGGACCTCATATTAAATAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAAGAG/G/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGCTCTTCCCATTTTACAAATAGGAGACAAATAATAGGAGATTAAATAACTCATCAC TGTTTTCAAATAAGGAGTGTGAGGTTTGTGCC

WI-1795b	130 T C ---	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGTCTTCCAGACTCCTACGATTAA AATTGTATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTCTTGCAGAAAGAAAGTTCJC GTCTACCAATTTTACCAAAATTCGTAGTACAAATTTAAGTATCTCTTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATT
WI-1795a	47 T C ---	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGTTCJCCTCCAGACTCCTACGAA TTAAATTGTATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTCTTGCAGAAAGAAAGTC GTCTACCAATTTTACCAAAATTCGTAGTACAAATTTAAGTATCTCTTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATT
WI-10616d	136 GA ---	---	---	CACACAATTTGCAACACTTCAAGTGAAGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGGTTTACTCCACGTCTCCATACGTAGTCTGGTCTCCTATCACAATTGCCA CIGAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616c	136 GA ---	---	---	CACACAATTTGCAACACTTCAAGTGAAGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGGTTTACTCCACGTCTCCATACGTAGTCTGGTCTCCTATCACAATTGCCA CIGAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616b	141 CT ---	---	---	CACACAATTTGCAACACTTCAAGTGAAGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGGTTTACTCCACGTCTCCATACGTAGTCTGGTCTCCTATCACAATTGCCA CGTAGCCTCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616a	116 GC ---	---	---	CACACAATTTGCAACACTTCAAGTGAAGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGGTTTACTCCACGTCTCCATACGTAGTCTGGTCTCCTATCACAATTGCCA CCACGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-1126c	52 GA ---	---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTCCAGTATCAGTGAATAATAA AAACCTGTAGTCTGCTTGCATTTTCAAGATTCAATATATCCAGATTGTTTCCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATAATTTAATTTCAAGTTCTCTCAAAAGGAATATGAAATTT TGTTAAATGCAAAATCCAGCTGTAACTTTTGGACTTGCCTTTATTTCTT
WI-1126b	230 T C ---	---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTCCAGTATCAGTGAATAATAA CCCTGTAGTCTGCTTGCATTTTCAAGATTCAATATATCCAGATTGTTTCCCAGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATAATTTAATTTCAAGTTCTCTCAAAAGGAATATGAAATTTGTT AAAATGCAAAATCCAGCTGTAACTTTTCTTTGGACTTGTCTTTATTTCTT

WI-1126a	97	T C ---				CTCTATTCTCTGGGCACTGCTTCTTTGGGGCAAACTCCAGTATCACTGATATAATAAAAA CCCTGTAAGTCTGCTGCAATTTCAAGATTC/CAATATATATCCAGATTTGTTTCCCGCAAGAAAA ATTTTATTTCTCAAGATATAAAAAATAAATAATTTAAATTTTCAGTTTCCCTCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACATTTTGGACTTGCTTTTATTTCTT
WI-11183c	124	C T ---				TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTC/ACTAACA TTTATGACATACAAATGACCAAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTTAAATATTGGT ATGGGGTCTAGAGTTAGTAATGGAA
WI-11183b	192	T C ---				TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTTAAATTC/ATTTGGT ATGGGGTCTAGAGTTAGTAATGGAA
WI-11183a	118	C T ---				TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCTTGTCACATAACA TTTATGACATACAAATGACCAAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTTAAATATTGGT ATGGGGTCTAGAGTTAGTAATGGAA
WI-10770b	174	G A ---				GCTTGGTTGGTTAGTCTTATGTCAGTCTTGGCTGCTCCCTTCTGCGCTGGCCCTTTGTATTTCA CCCATACCTGATGCTGCTCAGACCAATTTCCCTCTATCTGGAGCGCTTCCCTTGACTTTCTCCTG TTACCAACCTTCTTTTATCTTCAGGACACTCA/G/ATTCACATGCCACTCTCGTGACACTGCTCT TTCACATCTTCTGTGCTCCCTTTCCC
WI-10770a	49	G T ---				GCTTGGTTGGTTAGTCTTATGTCAGTCTTGGCTGCTCCCTTCTG/TCCTGGCCCTTTGTATTT TCACCCATACCTCTATGCTGCTCAGACCAATTTCCCTCTATCTGGAGCGCTTCCCTTGACTTTCTC CTGTTACCAACCTTCTTTTATCTTCAGGACACTCAGTTACATGCCACTCTCGTGACACTGCTCT TTCACATCTTCTGTGCTCCCTTTCCC
WI-9667b	82	C T ---				GATGACAACCTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCTGTATCATGG TTATCACTGGACA/C/TAGCCACCTCCCAGCAGGCTTAGAACTCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGCTACCCAGTACCTAAGTCCAAACTTGCATCT
WI-9667a	68	G C ---				GATGACAACCTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCTGTATCATG G/C/TTATCACTGGACACAGCCACCTCCCCAGCAGGCTTAGAACTCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGCTACCCAGTACCTAAGTCCAAACTTGCATCT

WI-10400d	189 A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTTCTAATTTT TCTTCCCTTACCTTACTCTCCCAACCAAAATAACGTAGTACCTATGTCTG G GCCATGTAG TTTTTGGTTCAATTTACTTGCANAATTATCAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---	---	ACATTTTATTAGCAAAATCAGCAAAATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTTCTAATTTT TCTTCCCTTACCTTACTCTCCCAACCAAAATAACGTAGTACCTATGTCTG G GCCATGTAG TTTTTGGTTCAATTTACTTGCANAATTATCAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTTCTAATTTT TCTTCCCTTACCTTACTCTCCCAACCAAAATAACGTAGTACCTATGTCTG G GCCATGTAG TTTTTGGTTCAATTTACTTGCANAATTATCAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---	---	ACATTTTATTAGCAAAATCAGCAAAATAAATAGAAAGTAATTGCAATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTTCTA ATTTTCTTCCCTTACCTTACTCTCCCAACCAAAATAACGTAGTACCTATGTCTG G GCCATGT AGTTTTTGGTTCAATTTACTTGCANAATTATCAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---	---	AAAGGGCTACAACTAAGGCCAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTCACCA C T T TAGAAAGGGCATTTCAAGCACATTCATAGGCTTCATATCTGTTAG CAACAAATGGAATGTATTAGCCCAAGGCGGGTATGACCAAAAGTCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---	---	AAAGGGCTACAACTAAGGCCAAACCATGA C T GGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCATTTAGAAAGGGCATTTCAAGCACATTCATAGGCTTCATATCTGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCGGGTATGACCAAAAGTCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---	---	CGAGCTGGGATAAAGCAAGGGGACCTTGGCGCTCAGCTTCCCTGCCACATCCAGCTTGTGTC CAATGAAATAGTACTGAGATGCTGGGCTGTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAG AAGAAAGACTGTCAGGAAGGGTCCGAGTCTGTAAACACAGCATACAGTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---	---	CGAGCTGGGATAAAGCAAGGGGACCTTGGCGCTCAGCTTCCCTGCCACATCCAGCTTGTGTC CAATGAAATAGTACTGAGATGCTGGGCTGTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAG AAGAA C G ACTGTCAGGAAGGGTCCGAGTCTGTAAACACAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTTCTG



WI-7038a	31	G A ---	---	CGAGCTTGGGATAAGCAAGGGGACCTTGGC[A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCAATGAATACTAGATGCTGGGCTGTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAAGACTGTAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCCTGCAITTTATGGTGTAGTTCTGA
WI-3429b	64	G T ---	---	ATACGTTTCTGTCTGCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCGGCTCCACACA[G/T] CCCTAGCCCCCTCAGCTTGCATGTCTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCAGCTCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T ---	---	ATACGTTTCTGTCTGCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCGGCTCCACACA[C/T]AG CCCTAGCCCCCTCAGCTTGCATGTCTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCAGCTCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A ---	---	ATTTAGGACAGTGAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAAGTGACGGTGACCT GTGAGCCCCATTCTCTG[A]TGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCTCTGGGTGCTCTATGTGCAGTTTCATCAT
WI-6786b	111	A T ---	---	ATTTAGGACAGTGAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAAGTGACGGTGA CCTGTAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCTCTGGGTGCTCTATGTGCAGTTTCATCAT
WI-6786a	106	A T ---	---	ATTTAGGACAGTGAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAATGGAATAAGAGTGAAGTGACGGTGA CCTGTAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCTCTGGGTGCTCTATGTGCAGTTTCATCAT
WI-6711b	226	G T ---	---	GGCTATTTGTAATGCTTGGTATTTGACTCCAAAATGATAAGTATGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAACTCACTGAAT TTCATATACCTCCATTATTAATTAATCAATCATATTGCAGAGAAAAGACACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGAATCTCTAAA
WI-6711a	36	T C ---	---	GGCTATTTGTAATGCTTGGTATTTGACTCCAAAATGATAAGTATGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAACTCACT GAATTCATATACCTCCATTATTAATTAATCAATCATATTGCAGAGAAAAGACACGGTGCCAACTG GGTTGGTTGGTGCCTGCACACCCACAGTGGCAACTAAGTGAATCTCTAAA

WI-10613b	172	A C	---			ATTGTATGCCAAATCATAATACCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTGAGCCATA TGGTGAAAAATTTAGAAAGTATTCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTT TTTGCAACTTTTGACAGGCCAGGCAATTTTATTTGACJGCCCCAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTCCACTCTATAATTTTAAGTCTCGGACTAGGAITAG
WI-10613a	44	G A	---			ATTGTATGCCAAATCATAATACCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAAGTATTCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGTTACTATAATTTAG AAGGCTCTTACCTCCACTCTATAATTTTAAGTCTCGGACTAGGAITAG
WI-7587c	133	A T	---			GCTCTAGTGGGAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCTTGAAGC ACATCCCCCTTCTGGATCTGAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAAJ/ TJGGAATGAACCACTCCCTGCCCATTCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-7587b	81	G A	---			GCTCTAGTGGGAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCTTGAAGC ACATCCCCCTTCTGGATCTGAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCCATTCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-7587a	28	C T	---			GCTCTAGTGGGAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCTTGA AGCATCCCCCTTCTGGATCTGAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCCATTCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-10681b	103	T A	---			ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCATTGACTTACGCAACTCAATCAGCAACC ACAGAAAAGCTAAAGACATCCTTTTAAAAAAGCCTTAAAGACAGCCATTTTAACTTAATTCG TAGTTTATGATTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATGTCTTGGAGAGGAGGAGTGACGCTCTGTAAAG
WI-10681a	41	A T	---			ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCATTGACTTACGCAACTCAATCAGCAACC ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAAGCCTTAAAGACAGCCATTTTAACTTAATTCG TAGTTTATGATTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATGTCTTGGAGAGGAGGAGTGACGCTCTGTAAAG
WI-7222c	126	G T	---			GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG(GT)AATAA AGGAGGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAGGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTT

WI-7222b	255	GA	---	---	GCCTCCTCAACTGTCTGGACCCAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAAATTCCTTGAACAAGAAGAACTGGGATAGTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGGTGTATTTCAAAGACTCGAATTCATTTCTCA
WI-7222a	126	GT	---	---	GCCTCCTCAACTGTCTGGACCCAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG(GT)AATAA AGAGGGGAAATTCCTTGAACAAGAAGAACTGGGATAGTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGGTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	CA	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTT(CA)TTATCTCCTCCAGTTCAAAATG CTTGATCTTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTGTAGTTTAGCCCTTTTCGGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAATAACGCCGCTTCCCTGGGCGTACAGAGATCCTTGCCCTT
WI-8054c	237	GT	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCTATCTCCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTCTTTGTAGTTTAGCCCTTTTCGGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCTTCC TGTCAATAACGCCGCTTCCCTGGGCGTACAGAG(GT)AATCCTTGCCCTT
WI-8054b	148	TC	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCTATCTCCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTCTTTGTAGT(C)TTAGCCCTTTTCGGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAATAACGCCGCTTCCCTGGGCGTACAGAGATCCTTGCCCTT
WI-8054a	131	CG	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCTATCTCCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAG(C)GA CAATCTCTTGTAGTTTAGCCCTTTTCGGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAATAACGCCGCTTCCCTGGGCGTACAGAGATCCTTGCCCTT
WI-10854b	152	GT	---	---	TTCACAAAAAATCTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAGCGAAGTTGAACACAGAAAGACGATAGTTAACGTCTGGTAAGTTAT ACGGTGTGCGAGGCAACAGTGGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTATCTTGTG TTTTAGACACAGGGTCTGCTGTGTTG
WI-10854a	102	CT	---	---	TTCACAAAAAATCTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAGCGAAGTTGAACAC(C)TGAAGACGATAGTTAACGTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTATCTTGTG TTTTAGACACAGGGTCTGCTGTGTTG

WI-9826b	127 G A ---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTGGTGTTCACGCGAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GCCTT CAAAGCCAAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGTCTAGATATTAA GGCAGAGAATCAGAAAGTTTGAA
WI-9826	125 A T ---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTGGTGTTCACGCGAGTTGAGCCATTGTGACAGAGGCTGTTA/TJGGCCTTC AAAGCCAAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGTCTAGATATTAAAG GCAGAGAATCAGAAAGTTTGAA
WI-15986	60 T G GTGGGTTTT	TTGTTTGTGT GTGGGTTTT	TGACATTATAT AAACGTAAAA GAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTGTTGTGTGGGTTTTTTTTT/GJTTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29 A G A G	AACTGCAAAAT AGGAAACCAG	CCACCTGGGGC TOOC	TTCAAGTAACCTGCAAAATAGGAACACAGAG[G/G]GGAGGCCAGGTGGGACAAATCATGGCTACCCC TCCCAACAGAACAGGGGGAGGAGGTGGGCCCTACACCCCTTAT
WI-8170b	259 G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAAGACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGCTCCATCAAGTGCAATCCTATCAATCAGAA ATAAGGTAAAGGGCCCTCAATGAAATCTACGGAAAAACATAACAAGA
WI-8170a	204 T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAAGACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGCTCCATCAAGTGCAATCCTATCAATCAGAA AT/AJAAAGGTAAAGGGCCCTCAATGAAATCTACGGAAAAACATAACAAC
WI-8172	136 C G GACA	CCTTATTAAAA ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTTCCAATCTCCAGGTACATGTTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCCTTTATTAATAATGTTTCTTGACAT A/C/GIAGTACCTTTACAGGTTATACATTTCTCTCACCGTTTACA
WI-8183	56 G A TGC	TGAATAAAA ACAATTTCTGT	TGTTGTGAAT CAAACCTGC	AGCAGGGTTTGAATTTGATCCCTTATTTTACATGAAATAAAAACAAATTTCTGTTC[G/A]GCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTCGTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83 C T ---	---	---	GCCTTATTGGGATTGCAAGCGTTACAAGTTAAAGACAAAAACCAAGCATGGGATTTTGC CGGAAAT ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAAACACGGG
WI-8712	44 G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCACAATGACACTGTGTAAACAGCACAGGGAAGGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCTG TTCTTAACAGCAGAGGCCAGCAACCTAGAGCGCCCTACCTAGCCCTCTAAT

WI-8827	22 C T A C T A T G G	T C C C C T G G G A G	G C G A T T A G G A T	GGTGTCCCTGGGAGACTATGG(C)TGTAGTAACACTAAATCCTAATCGCCATGCATTGGAAATTATT CCGACTATTACTTTCTTAGTTCCTTTATCCACCCAGCTTCT
WI-8833	51 A T A T T C T C T G	T C T C C A T G C C	C C T C A C A C A T T	CTCCGGCCTCTAAAGCTCTCTGTAGACTGTCTTCCATGCCATTCTCTG(A)TJGCCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G ---	---	---	ATTTTTAGCCATGTGGTAAAGTTCATTTTCAGTACATGGGTAAACCCAGGCCCTTTCCCA/GJT TATATCCAGGTATGCTACAAAGTCTTTTAACTCTTATCAGAAGTTATTACTGTCTTCCCTAGAGAG GCTACCAGGCTAAATTCACITTAGTTGGTTGTCTAATGTCTCATTTATTCCTGAAGCTCGTG
WI-8850	21 A G C T T T G G C C T	G G G A C T T A A C	C A A A C A G C C A	GAGGGACTTAACCTTTGGCCTAGJCCTGCCCTGGCTTTGGCTCTGGCTTGTCTTTTGGTTTCTT TCTCTTCTACTGGTCTTCTTCTTGTCTTTGCCAGCCACTAIGCTGT
WI-8853	79 C T A G G A T A	O C C G G C A T T G	A G T C T T C C T G A	ACTTCTTGAGCTGAGCAACCTCATCATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CAITGAGGATAIC/ATGGAAGGCTCAGGAAGACTTTCATTCTCAA
WI-8865b	52 A G ---	---	---	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCTGGTGGAAACA(A)GJACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAAA
WI-8865a	42 T C A	C A C A G A C T G A G G A A G A C A G T	G G T A A G T C C G A A G C A T G T T G	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA(T)CJGGTGGAAACAACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAAA
WI-8895	32 A C ---	---	---	GTGCCACAAACCTGGACACCACCAACAGAAAT(A)CJCTCCCGTCTTTGAAATTTCCATTAAGAGCA CAATGGGGTAAATTATACCAGGGATGCTCCAATGGCTCTTTC
WI-8456	93 G C ---	---	---	CCTTTAAAGTCACAGTCACTGACTGTGGACTGATATTTGTGAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA(G)CTTATGTCAAGTTAATAAACAATTTCTAAGTGTCTCACTC TCAACTTCTGTATTCTTGGCATGTCCAGTAACAGTTCACAGGAGACACCACAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACTCCCGTCTGCTGCTCAGTCAACCAC
WI-8496b	157 A G ---	---	---	TTTCATCATCAAAAGTTTCTTCCATAGAAGAAATGGTAATGTGTATCAGTGCATATTCTATGAAA ATTCAATCTCAAGTAAGCTAGCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA(A)GJTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A ---	---	---	TTTCATCATCAAAAGTTTCTTCCATAGAAGAAATGGTAATGTGTATCAGTGCATATTCTATG AAAAATTCATATCTCAAGTAAGCTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G C C A G C	G T G C A G G A A G	A A C G G C A G G A I G G G A	CTGCAGGTCTATGTGAGGAAGGCCAGC(A)GJTCCCTCTCTGCCGTGTGTACCCACATCCACAGAGCA GCCCTAGTGCAGGTGAGCCACTGCCACCCACGGCACACGGGAACAGGCCATGCTGC

WI-12108	40	C T A T A	TGGAAGGG TAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC/TJGAAATACTTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTITAA
WI-5989	29	G A C A G G C A	CCACAAGGT CACAGGCA	GGGTATAACAG AACCCTATGTA G	CAGGCAACGTCACAAAGGTCACAGGCA/G/ACGTACATACGGTTCGTATACCCCATATATTAC CCCTCATGTCTAAAGAAGACATTTTCTCTTAGAGATTTTCATTTAGTGTATCTTTAAAAAAAAT CTTGTTAACTTGCCCTCCATCTTTTCTTGGGTGAGGACAC
WI-12201	61	C T C T G C A T G	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGCTTTTAGCCCTTTTCTCTGGAGTGTATATGTCCTCAAGCCCATGTATACCTGCATG/C/TJGCCA GGTATGGTGGTGGGGTGTGATGGACGTGGGTTGCAGCCCTCCACTGCTGATAAAAAGGC
WI-12018	31	A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTGAGGAGCCAGCTGTGACTT/A/TCTCTCTGTTTCTGTCACTCTCTCCCCACATACCA ACTCTTACCATGATGATTATACCAATATACAGTTCCTTATATAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCGAG
WI-14162	57	A G C C T C	TGGCTCGCTG CCTC	AGGGATCAA GAGAAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAAGAAACCCCTGGCCTCGCTGCCTC/A/GJGCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A G T T	CATGCCCTTTA AGGATTAAGT G T T	TCCTTTCTCTT TGGTAGTGG	AGCATGTAAGGAGCAGTTTATTTGATTGGTATATTCAGGTTTCTAACCCAGCTGAAAAATTTCAAATA CATGCCCTTTAAGGATTAAGTTTAA/GJCCACACTACCAAAAGAGAAAAAGATTTATATGATCATCAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C A A T T	GTTGAGTATT GTTCTGCTCAT T C A A T T	GGAAGGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATATTCTGATACACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCAATTAGTTGAGTATTGTTCTGCTCATATAATTJ/CJCCAATATGTACCAGACCTTCCC
WI-12326	25	G A C A	GACAGACTTC AAAAGCAATT C A	AGGTTTGA TATGATTTAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC/G/AJCTTCCAGAAATACAAAGTACTTAAATACATATTTTCAAAC CTGTTTGCAATTCAAACAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T ...		...	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTCAGCATATGTATTATJ/C/T TGAATAAATTTACAAAAGTGGACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTATTACC
WI-11305	87	C T A T C A C A C C A	CAGACACAGC TCCAAATAAT T A T C A C A C C A	GAOCCCTCCGT G3GC	ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAAGGAAAGGACAAAGTACCTTTGTATAGAAATAT ACAGACACAGCATCACACCA/CJTAGGGCCACGGGAGGGTCTGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	A G T T T T	GGGAGGAAAA TCCAAATAAT T G T T T T	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGTTTCTGGTGAATCTTTTAAAGCAGGGAGGAAAAATCCAATAAATTTTTTTAAJ A/GJAAAGTTTAGCTATCCCCAATGCTATTTAATACAAATTGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGOCOCG
WI-11324	40	C G T G T G C C C A	GGATAAATCA T G T G C C C A	ATCAAGCTTTG GGGCTT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCA/CJGJAGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTATCTGTCTGTGTC

WI-11352a	69	T C G	AGCAGACAG ATAGTGGAAA	GACCTCTGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAGGAGAGAGATCATCTACATAAGCAGACACATAGTGGAA AGTCGCTAGTGTCTCTACGAGAGGTGAGATCATATCCATAGAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTTGGAG ATTCTGATTCA	GGCCCGCTGA GCAC	TTAGCCCATGCTGTCAATTGCAATCACCTGTGAACCTATGAAAACTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGTCGTCAGGGGGCTGGACATCCATGTTTGGGAAGAGTTGCCGGGT GAITTCGATGCGTATAT
WI-11385	75	T C G	ACAGAGAGCT TTCATATCTT	GATTCATCT AGTCATGGTCA	CTTAAAGCATTATAGTTGGCTGATGGTGACACAGAGACTTTCATATCTTGTTTTAAAAAGTC TCTTCAGTCGAGGAAAAAGCTACAGATTAAAAAATATGACCATGACTAGATAAGAAATCAGC
WI-11388	88	C A A G T T C	TGTTTGAAT ACACGTAAC	TGCTTGTATC CAAGTTAAAT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGGAGCTCATAAAAAATTAAAGAAATGAATGTTTG AAATTACACGTAACTAAGTTCGATATAATTTTAACTTGGATACAGGCAATTGTTATGCTAAT
WI-11392	55	T G A T A A T A C	GGTATGTGT CTTGAAGTTA	GTACATTCAG TGTTTGTAAA	TTCTATCATTCCTTAAATGGGAGGTTATGTGTTCTTGAACCTTAAATAATACTCGCTTTTACA AAACACGTGATGATCTTCTTGTGAGAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTGTGTTT AAATGGTGT	AGCTTATTT ATATCACCCA	AAAGAATAAGATGGCAATTTTTCAGTTAAATTTTGTGTTTGTAAATGGTGTGTTTATGATGGGTGAATA TGAAAATAAGCTTACCTCATCCCACTCTAAAAGGTAGTTGGTGAATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCACCAAC CAGC	TGCCAGGCGT TATTTG	CTGTCAGCTTCTCCAACTAAACGTTCCAGTATGCTGGCAGCAGCTGCTGCTGTTCTTGGTG TATCCCATTAAGTGAATCCCAACCAACAGCAGCAGCAATAAGGCCCTGGCACAAGTAAGCTCTCC ATTTTGTAGAAATGAAT
WI-11466	26	C T T T T A T T T T G C A	TGAGAAGCCA TTTATTTTGA	GTTTATGTTA TAAAAATGAC	ACTTGAGAAGCCATTTATTTTGCAGTCGCTTCAGTCCAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAATCTTCTATTTATCTATTTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G	---	---	TTTTCTTTTGTGCTCTTTTTTTTAGTAGAAGCAGGAGGGAACAGTTGTCAATACTACCTTCTGTTGG TCCCTGTTAGACACATACCTTTCTTTGAAATGIAAAATGCA
WI-11276	41	A G A G C A G A C	GGCAGOCAGG AGCAGAC	TGTAAGTGA GGCGGTG	AGGCAACACTGCTTTATAGGCGGGCAGCCAGGAGAGACAGCAGCAGCAGGCTCCTCAGTACACATT CCCAACCCCTGCTCGGTGCTCCCACTCAGGCTGGGCTGGGCGGAGCGGTAGGCTGGA
WI-12210	76	A G A	ACTGGGAAA CAACTATTGC	TGCTAGTTGC ATATGTTTCC	ATTGGAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATACTGGGAAAAACAA CTATTGCATAGGGAACAATATGCAACATAGCATCATTTGCTCTAGA
WI-14186b	88	A G	---	---	AATGCTGCTGTTTATGAGAAGCTGTTGGTCAATTTGATGGAAGACACATACGGGTACAAAATTACA GGTGGTTAGTTCATTACATGAGTACAAATCAATTAGAGCTTTACAAGTCAATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCAITTTGAT GGAAAGACAC	AACATAACCA CCTGTAATTTT GTACC	AATGGTCTGGTTTTATTGAGAAGCTGTTGGTCATTTTGTGAAAGACACATAIC/TGGTACAAAATT ACAGGTGGTTTAGTTCATTACATGATACAAATCATTAGAGTCTTTACAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTTTTTGGCTATAGGTCAGTGGTTCTAAAACTTGAGCTTGCAAGAGAACACACTTTGTGGGCTT[A] GTTCAACATGGACTGATAGTCCACCCAGATTCTAAGTGGTAGGCTGGGGTG
WI-12345	37 C A	GTGCAAGAA AAAGAGAA	TTGACAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGAA/C/A/CCTGAACCCCTCTGCAAGTATTCTCT TTCCTGACCAGCTGGGCTTGGCACCTTTTGAGATTGCAAAA
WI-13416	71 C A A A A	AAATTTTGG AAGTTTTTCAG	AGTGTATAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTTATTTTCAAAATTTTGGAAATTTTTCAGAAAAAATAAATGACAAGAACA CATA/C/A/AAATATTGAAATTTATTCATTGAACATATAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46 G A	TTATCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTGGGTCT AAA	TTTGAAAAGATGCTGAATTTTATCCCAAGTATAATTTTAAAAGCT/G/A/TTTAGGACCCAAACATA TTTAAACATCTCTTACACATACAGAAATTCAGTTTACAAATATCCAGAAAGGCAATTTTCTTAAGCAG T
WI-12086	72 C T	CCGGGAAAC TTGGATT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATGGAGAAAGAGTGTGGACACTGTTTACAACAAACGTTTCCGGGAAACCTTG GATTT/C/TCCAAGACCCGAGACTCCTCCAAAGTTCTCACTGTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCTTAGCT
WI-11549	102 T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGCTCTCACAGGTGTATTTTGTAAAGAGTTGTCTATCTAAATTTTCATATTTATTGGCATAAAGT TCATAATATCTTTTATGATCTTTAAATATCTG/T/G/GGGGATTTGTACAGACTTTCCTC
WI-11585	79 T C	TGGTTTGCAA AAACAAA	CCATGCTTAC TGATACTTC	TTAGAAGGAAAGAAATAAAACACCGTAAATGGGAAATATCAGTTAGAGGTAGGAAGGAGCTGGTT TGCAAAAACAAAAT/C/GGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAAAGAGCAGGGGTAGAGT T
WI-11604	68 G C	---	---	TTAGTTGGTTTCTGAACTTTATGCTGTTTATTTTAACTAATAGGATGTTCCAGTTACCAGCATTT G/C/JAGAACTAGGGACTTTTCCATGAAAATAATTAAGAGCTAAGGAATTCGACGCTCACCATTTC TTTGTACTCTGCAGTT
WI-11614c	108 C A	---	---	CAAAATCAAAAATTGAGGAGGCAAGACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCCACTGGACTTGCCAACTTCACTGTGAAACTGCA/C/A/JATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTG	AGGGTGGGAA ATGOC	CAAAATCAAAAATTGAGGAGGCAAGACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG/A/G/GG CATGTTCCCACTGGACTTGCCAACTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83 T C	---	---	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGGTACAGGATAATATACTCAG ATATTTTAAAATAAA/T/C/TACTTAATAAAGAAATTAGCCATACCACATGTTCCATTGCTAC AAGAACAAAATTGGCAATGA



WI-11626a	39 G A G	TCCACTGGAA CATGAAGGTA	GGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTCCACTGGAACATGAAGGTAG[G/A]GATAAGGTGTACAGGATAATATACT CAGATAATTTTAAAATAAATTACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAAATTGGCAATGA
WI-11627	23 T C	CCTTTCCTCC ATTGTCCTC	CATTTGCAACG CATCTCAAG	ACCCCTTCCCTCCATTGCTCTC[T/C]CTTGAGATGGGTGCAAAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTGCGCATGTCAAGTCCATCCATG
WI-11638	61 A G	GGACTTAAAA AGATCTGCTTA T C C T	AGAACTTGGT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCT[AG/TA TATCCACATAACTCTAGTGTACATAAAATAATTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTGGTA
WI-11537	119 C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAAAATAAGCAAACTGTGAGTAAACGAGGCGAGCTGAATAAATTACAG TATACAATATTAGAGAATATTATGTTGCAATTGCTCATCTTACTCTGACCA[TC/G]ATAATCATTTCTT TTTGCTGGGTCCAGGACC
WI-11654	37 G C	GCCAAAAGAC TATTCAGCAA C T G	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTACGCAACTG[C/A]AACTGTCTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATACTACTACTCAGAGTTCACACTCATATTTTCATATTTTT ATTTTGGGTGTGGGT
WI-11656	28 G A A A	ATTGATTTTAG AAGGAAGTGC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAAGTCAA[G/A]CTTTACTTGAGGACAAAGCCTTGCTGCAGTTGTTT AAATGTCTCTGAACAATCAGATCCCGAGCCTGGAT
WI-11680	55 T C	...	...	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCCTTTT[C/TT]GCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47 T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAG[TC/A]AGGTTGGCTTCTCTA ATGCCACCATCTTGTTGTTTCAGAATCTTTCCACATCCGCC
WI-11702	69 C T	GAATAATACT GAAATAACCA CAGCAG	AGAACAACTT AAGCAAATTAT ACTGAAA	TTACATGGGTCAATGGTGACATACTTTCAATAATTAAAAATCGAATAATACTGAAATAACCAACAGC AG[C/T]TTTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAAATTTTGTCTGCAGA
WI-11706	60 C T	TGGCTGGAATT TTCTCTCTT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAAATTTCTCTCTTGTAACAATTTATTTGC[CT]GGCTG GAATTTGTTCTTGGTGATTTGCCCCCTTGCTGCT
WI-11709	105 T A	AGAAGCTTGC TTT CAGTTTGC	TCATTTCTTCT AATTTTACGGG A	AATATCATCATCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTGGCATACTCATC TTCTTCAGGACACAGAGAGAAAGCTTGCTTCAGTTTGC[T/A]GTCCCCGTAAAATTAGAAAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103 C A	GCACTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCACACAGCCACCCACTCTAGACACGCCCTTCAG TCCAGTCCATTCTGGCACTAGCCTCAGTCTTCACTCAG[CT/CT]CTCCCTCCCTCCACACACTCTTC

WI-11715b	123 C T	AGGCTGGCTGC T AGCTT	TCCCCATCCTG TGGCT	AGAAATGGAGCTGTTGGGGAGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAG/AGGAAAGAGGCTGGCTGCAGCTTCTTAGCCAC AGGATGGGACTGGGAAGA
WI-11715a	49 A C	AAACAACTCT AAACAACTA TAAACAGAC A	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGGAGGGACATGCACACAATGTAAACAGACAAA/CITGCAATTACAACTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTACAGCCAC AGGATGGGACTGGGAAGA
WI-11727	43 G C	TCAACA	CCTGTGGTTG TGTTCGAG	CTGGATTTCTATACCTAACAACTCTTAAAAAACAATCAACA[G/C]CTGCAACACAAACCACAGGC AAAATGAAAAACAGATGCCAGACAGCACCCACACATGGCACACAC
WI-11728	16 C G	ATCTGTGGTTT TCGCTG	---	TTTTATTTATCAAACT[C/G]CAATTCATTTTACAAATGTAAGTTATCATCAGCTCCCAATCCACTTT CTCCATCTCTATCTTTCCACCTACACTTTCTCTCCCTACAAACCCGGGTTCCAA
WI-11758	61 A G	GCCTACAAA GTATTTCTAA AATATAA	TGATTGGCCT GTTGCTA	TTTTCTCTTTTAAAGTCGGCTATCTAACTAGAGGAGAACTGTGTGGTTTCGCCTG[AG]TAG TTTTCCTCTTTTAAAGTCGGCTATCTAACTAGAGGAGAACTGTGTGGTTTCGCCTG[AG]TAG ACCACAGGGCCAAATCAACACAGCTTCTTTAGAGAACATGGAGTGCACAGATCCACATCA
WI-11295	37 A G	GCCTACAAA GTATTTCTAA AATATAA	AAAAGTGCTCA TCTGTGAATC T	CCGGCTCACAAGTATTTCTAAATATAATTTGCT[AG]TAGAGTTACAGATGAGCACTTTTCA CAATAGGTATGCAACAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93 T C	---	---	AGCATGATAATCTCGCTGGAGTTTCTGTAGCTCAGCAACAGCAGAGTCAGAGATTAAGAATT ATTTATGGCTCCTTTTTTTCCCT[C/G]GTGATTGTTAATTAGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G	GGCTCAGAGA GCAAGGAA	AAAACCTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTATTAATGGCTCAGAGAGCAAGGAA[C/G]CACACAAAAATTTACAGCTGA GTTTTGGGCGCAGAGACCCCTCTCCACCTTTTTCATGCCTGTGTGTACACACACACTGTCCAAGCCTC AGA
WI-11790	28 A G	CCCACTTACC AAACCTCTG	CSGTAGGCGAG GCTAAGC	TAATTCACCCAACTTACCAACCTCTG[AG]GTAGCTGCGCTACCGTACACATGCTCAGAGCAC TTACATTAACCTACAATGGGCAAAATCACTAACACAAAGC
WI-11879	61 C A	AGTATACA GGTATTAGAA	GATAGTTGAAC CTCTTCACTTT ATAAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTCTCTCTTTTATTAAGTGAAGAGGTTCACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T	GGTAAATGT GGTATTAGAA AAGTTTAAA	CAATTTTCAGA TTGCTATAGC AAAC	TTTAAATTTTCCATTTCTCCCTTTTATAGTTTTAATGTGGTATTAGAAAAAGTTTAAATTACAT ATGTGGCTTATATTCTATTCTA[C/T]TGACAGCAGAGTTCTTCAAAAGTTTGTCTATAGACAACTGA AAATGGGTCTGAAC
WI-11906	52 A G	TGTTATAACAT CAAGAAAGA GATCTGAA	TTAATTTCTGC AGTTCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAAAGAAAGAACTGTAAT[AG]TGAGGGAACTG CAGAAATTAACCTTTCAGTCTAATTCAGAAATGCCAGAGTAAGATGAACCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CTCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTGTGTG GGTGGTCAAGTGGTATTCAGAAATCTCAGAGGAGGACAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATGGCCCAAGTTTGGCAGGCATGAAGAGTGGGCGAGTTCA/T/GGTT TTATTAGTATAIAAAATGGCTTTACAGGAAGCATTTATGG CCCTAGTGAATACAAACCTTTGTCTGGAGAC(CA)CCAGCTAGTCTAAGAAACTTCTTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAAGGGAA
WI-11946	31 C A	---	---	ACAAAAATCACAAGTACAACACTGCTTATTTTCTGCTTGAAGATCAGATCTCTGGTTATTTAA/T/ GATCAACATTCACCACACAGCTGAAGGAAATTAACCTGAACCT
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT GATTT	CAGCTGTGGTG AATGTTGAT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAACAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAAT/A/AAATAAAATCTGTAAACATTTCTCATTTCTGTACGA ATACTTTCTTTTGATATTGCAATCTATGGCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11027	90 T A A	---	TTTATT	TTCTGCTGAAGATCACAAAAACAATTTCAACCTCTGTGGTTCAAAATAATTAAGGATCTTGACCTTT GTGTTATTTCTGTTTCAACTAAGGA/C/TAGACTTCAAGAGGCATAGCTTCCCTGTGAACGTTTTT AAACATCTTTTTCATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-11049	95 C T	---	---	CAACATTTATCAACATGGTAGGGAAAAGTTCTCACTCTGCACCTATAAAAAGGACAGCCAGATATCA AC/C/TGTTACAGAAATGAAATAAGATGGAAAATTTTAAACAAATTG
WI-15488	69 C T A C	AAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTAA/GIGTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACCTTTTCCCATTTTACAGACAAAACCCAGT ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAGGAGCTAGGACAAATCTTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAATCAGCAGCTATCTTGGTGCAGAGAGGTACTCCAAGTA C/C/TGTGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCCAACAGAGGGAA
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAGGAGCTAGGACAAATCTTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGTGGTGCAGAGAGGTACTCCA GTACCGTGGGGTCTTGATGACTTCCACGGTCACTGGGGATCCCAACAGAGGGAA
WI-11070a	110 G T T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	AATCTTTATATTTCCAGCTTTGAGCAGATTTTGTAGGGCTGATTTACCTCTAGCGGCAACCC AGAGCCAGCTATTAAAGCAGCCAGAAAGCTACAGTAATTTGAATACATGACCAATTT/C/CTCTTTTAGC ACGTTCTTGTCTCTC
WI-12020	121 T C	---	---	---

WI-11076b	142 G A ---					CATGGTCTGCCAGCTTACAGGAAGCATGGTGTCTGGCATCGGCTTATCTTCTGGAGGCCTCAGGAAG ACTCTGAATTTATGGCAGTAGGCAWAGGGGGAGCGCATGTACATACCCAGAGCAGGAGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAATCCTACTCTGTCAT
WI-11076a	106 T C AGGCA	AAGGGGGAGC	TCCTGCTCTGG	GTATGTGAC	GGTATTCAAA	CATGGTCTGCCAGCTTACAGGAAGCATGGTGTCTGGCATCGGCTTATCTTCTGGAGGCCTCAGGAAG ACTCTGAATTTATGGCAGTAGGCAWAGGGGGAGCGCATGTACATACCCAGAGCAGGAGAGAGAG GAGAAAGAGAGGAAGTCCACACATTTTAAATGATGAGTTCTCTCAAGGAATCCTACTCTGTCAT
WI-14263	49 T C GGCATATTCA	CGCAGAAAAA	AATTAGTATGG	GACA	GGTATTCAAA	ACCTTTAAAGTTTCTCCACCTACTCCCGCAGAAAAAAGGCATATTCAATTCGTTGCCATACTAAAT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAAGTAACA AATTATGCTGAAATTAGGAAGGGAGCATTCGTAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGCAAGCAAGTACCATTTTCCAAAGTATAAAACTCGTA
WI-14267	28 T C ---	CTTTTCATTT	TGATGATGCA	TACTATAAA	ATCAAAAG	GATTTGTTTATTCATCTCGCTTTTCAATTTTGTCTTTTAAATAGAACA[G/A]CTTTGATTTTAGTA TATGACATCATCATCATGAATTTTCTCTTACTTTGTATTTAGGCTCCACTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-15288	108 C G TTCCCTCTCTC	CATGAGAGGA	AAAAGCTTCTT	TCCTTTGGA	AAAAGCTTCTT	ACCTCTTTCTGATGACACTGTACCTGTAGGGGTCTAGAGAGAAAGAGTAGTAGACTCCTACTTTGCG TACAATTCAGGATGCAGGGCATGAGAGGATTCCTCTCTC[G]TCCCAAGGGAAAGAGCTTTTGGC AATAAATGGAGAAGGAGTGAACAAGTAATGAACAAACAGACCCAGATCAGAGGGAAGAGATG GCTTCTTGTTAATCTGGAGCA[G/C]ATTCAAGCAGCAATATTTACTGAACACTTGCATGTGCTG
WI-13951b	88 G C ---	GGAGTGAACA				G AATAAATGGAGAAGGAGTGAACAAGTAATGAACAAA[G/C]TAGACCCCGATCAGAGGAAGAG ATGGCTTTCTTGTAAATCTGGAGCAGATTCAAGCAGCAATATTTACTGAACACTTGTGTATGTGCTG
WI-13951a	39 C T CAAAA	AAGTAATGAA	TTCTCTGATC	TGGGGTCT		G GAGACAAAAAAGGCTCTTGCCCAT[G/A]ATTTCGGTCTCTCCCTCCTGACTGACCCAGTGTTCTT ACAATGAACATCCCTCAGCCCCATGGCATGGTGCATCCCTTCTCTTGGGATCTGTGAATATAAACA ACTGCTTGTCATGCG
WI-13264	25 G A TTGCCCAT	AAAAAGGCTC				TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[G/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAAAGTACTAATGTTTACTGTCATTTCCCTCACAAGGAGTTGAGCCCTAGATGAC
WI-13960	39 A C TGATAGA	AGCAAAAGGA	CATGAAAGGA	CAAAATTTGCAAT	C	AACCTTTATTTAGTACGCCCCAGTGACTTTATGTCATCTTATAACCAAGAGCCCTCAG[C/T]GAG AGCAAGTCTGAGCCAGAGGTTTATCACACTTTGCTCAGGGTCCACCAGGAACCAAGGCTTTGGCT
WI-15843	62 C T CAG	ATCTTATAACC	CTCTGGCTCAG	ACTTGCTCT		

WI-13983	52 G A	TCTCTCCCACT CCCTAAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAATATGCACTCACTGACTTACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13950	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTCCTCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGGTTTATTTTATAGATTTTTTAACACAGCCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAGAATAAATAAGATGGACTTGCAGGTGTAAGAGATTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTCTCTTGGCAACTATTCATTATTGACCACTCTTTTC CTCGTCAAGTGACCTGCCCATCATCAAGAAAGGCCCGGAAATATGAGTGAGACTCA
WI-14284	55 C T ...	...	...	ATTTCAACAAATCCAGAACAGGTTCTCACACITTTGAGCCCTTTAGTGCACAAACAC[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85 G C	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAGAACGCCCTGTCTATATGAAGACAAACAGGTGGCCATACTTGGGTGGAGGGATA CCGCTGCTATTCACAGAT[G/C]AAGATTGGTGAAGGAGACCATTGACAGATGACAAACGG
WI-13522	33 C T A C A C	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCCACTAATACAACTTGGAGAACCACTGACTTCAAAATATTATGAGAG AAATTAATCCAGGGAAATTTTGCAGAGAAGATAATA
WI-13529	42 T C T A C C A	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCTATCCACAAACATTTATTGAACAGTTACCAT[C/A]AGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCTCGAGGGGTTTATAGTCTAACAGGGGAACAACTCTC A
WI-13859	84 G A ...	...	...	TTATTTGTCAGAAATTCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]JACAAACAAGTATATATTCAGGAAAGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29 T C ...	...	...	TGAAAGGATACAGAAAAAACTCAGCGAAGT[C/G]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCACTTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTCTCAGCA
WI-13373	52 G A ...	...	...	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AAGTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCTTTGACGCGGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAAGAGCT
WI-13477b	61 A G ...	...	...	TTGGTTTTTAATACCTCTTGTGGATAAAGGACATTTTTCATTAGCTTGTCTTCAA[G/G]GAC AGAGAAATAAGATAAATACCTTAAGAAAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32 A G A G G	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTTGTGGATAAAGGAG[G/C]AATGTTTTTTCATTAGCTTGTCTTCAAAGAG AGAGAAATAAGATAAATACCTTAAGAAAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTTAGCAATGCAATTTATTTCTGGCAATAAATTAATATATGTCAGTTTATAAAAAAT GTTGGGTACTTTTTTCCAAAG[A/T]AAAAATGTTTCTGAAATGTGCACACTAGAAATATATGCAAAATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGATTACCATTAAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[T/G]ACCAAAAAAATTAAGATTTTTTGGGACAATTACATGTTT AAAT
WI-13582	43 C A AGACTGGGA	TGCAATCTAG	TCTGCGCAGTT AGATTCCA	AAGGTCGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAACTCTAACTGCGCAGAG AAATCAAGACCGATGGTGAAATCTGGGCAGCTTCAAAAATTTCTGCCTCCTAAAAACAATTTTCAG CCAATTTTTCATTAATGGC
WI-13857	28 A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAAATTAACCAAAATGT CTGCCCATTTTGTGTAGCTTTTACAGTACAGATTTTCATTGATGTGCTGCCACATCTG
WI-15809	77 T G TGTAATGCC	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGT GTAAATGCC[T/G]TTTACAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT TTAATCAGTCTGTGTCAAGAAAGAACAGGACTTGATCAAGCTTCCAGCCCTCACCACCTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTTGTCTAAACCAGAGAAAGAA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15892	123 A T ---	---	---	TCITTTATTCAGAAATGGAGGGATTTTCATTTGGCTTGAATGAGAAAGCTTCATCTCCACTCTA GCTGCAGTAATACT[T/G]GCATCCCATCCACTCTTCTCTCTTTTGTGACTGAAACTCTTCAAAGAACT GCTGAATGTCTCTCTC
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATTCAGAAATGGAGGC[G/A]CATTTTTCATTTGGCTTGAATGAGAAAGCTTCATCTCCACT CTAGCTGCAGTAATACTGCATCCCATCCACTCTTCTCTCTTTTGTGACTGAAACTCTTCAAAGAACT GCTGAATGTCTCTCTC
WI-15801a	24 G A AATGGGAAGC	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	GCTCGTAATGAGACAGAACGCTACAATCTGTCAACACTGGCTGGACACTGCAGTGA[T/C]AGGG GCAGGTGTGGGCGAGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA TTTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACC[T/A]AGACAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTGATATTTTGTCTTTTCCCGAGGGCAAAAAGA GAGTCTCCAGAAACCTC
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAACTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCTACTCTCTT GAGGTCCCT
WI-13789	62 G A AGGGAG	TTGGATGGCTG	CAGTGGCTTC CTCTGTTT	AATAACAAGTTTAAGTTCGAGTGCATGTTGGCAATGCAGGTTTTTAACACAGATCACAAAAAGC G[A/T]GCACAAAAAAGTACTGGCGCAAGGACAAATAATGCTAAGAAATTAGGCCAAACAGCTGC
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCCTTGGGCA GTACTTTTT	

WI-15625	40 C T ...	...	GTTCCTCCCACTACTCCCGCAGAAAAAGGCATATTCAATCTTGTCCCATACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACCAG COCT	GTCTCATTCTTGTCTAGGCTGTAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAGAA/C/GJAGGGTGGGTGGGAATACTTAATCAATATTTTGTGGAATTTACCCGAT GAAATCCAGTTATCTCT
WI-13600	26 G T	TAATGAGCC AAGCATCCAT	CTCACTTTAATGAGCCCAAGCATCCATG/TJCCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAACAAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA ATATTAAT	GATAGGAAAAGAAAGATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA/G/TJAAATCTATTAAATATTGTCATGAGGTATGCACCT GCOCA
WI-13650	76 A T	AAAGATTGAC AATATTTCACT TTTAAAC	GCATTAAACATTTAAAAATTTCTGAGGGATATTGATGAGAACTATGATGAAAGATTCAACAATTTTCAC TTTTAAACATTTAAAAAATACTCTTCATATCCTAGCCTGATGACTTAAAAGTTACCGG
WI-14319	83 C T A	CAATTCAGG CACAAAGCTA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAGATATAAAGGAAATAGCAATT CAAGGCACAAAGCTAAGCTACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAATT
WI-13528	80 A G AAA	CAATACATTT GCATTTTCTTA AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAAATCAATACATTTGCAATTTCTTAAAA AAAGAAGACATTTAGTTTCAGAGAAACCTGIGGTATCATGCAGGAAAAGCAGAAAAAAATTT
WI-13909c	93 A T ...	...	ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTCCAGTGAAGTTTCTTCTCACACT CTCTTCAAACTCGAATATCTTTTTCATGAGATGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAACT CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTCCAGTGAAGTTTCTTCTCACACT CTCTTCAAACTCGAATATCTTTTTCATGAGATGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A ...	...	TTTTTATTGAATTCCTCAATGTAGCAAAATCATTAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAACATCAITCTGGACIC/AJATGGAACTTGAAAAGGATGGCAGTGGAGACCAGTAACATA
WI-14323a	78 T C ACATCA	ACAGAAAAAT TAAGAAATCAA GTTCCCAT	TTTTTATTGAATTCCTCAATGTAGCAAAATCATTAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAACATCAITCTGGACCTTGGAACCTTGAAAAGGATGGCAGTGGAGACCAGTAACATA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA TCCCACACTT	AAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTTGGAGACTACCATTTATCAATTTTATATGT AATACACTCATCCAGATAATGAACATCTCGGAAAAG/AJAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33	G A T C	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGGCTTTTGTCTG[A/J]TTTGGAAAGACTACCATTTATTCAAATTTATT ATGTAATAGACTCATCCAGATAATAGAAACATCTGCGAAAGAGTGTGGGAATCACCTCATCTGTGC TGTAATCTGCTTACAGTCCCTTGCAGAGACACATATGTTTTTGCATAAGATATAAATTTGCTTCAT TTTAAACTAATTTAGTGT[T/C]TTTAAATTATATGAACCTTTTGGTGAATTATGAAGTGTACCAAAAC C
WI-15747	88	T C A G T G T T	TGCTTCATTTT AAACTAATTT	CATAATTCACC AAAGTTCATA TAATTT	AAGAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCTCGTTAAGTGTGGATATACCTTGGCTTGCA[C/J]GGACACCTTTTACG GAGGATTCGGGACAACT
WI-13752b	117	C T ...		...	AAGAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCTCGTTAAGTGTGGATATACCTTGGCTTGCA[C/J]GGCTTGCAACCGACCTTTTACG GAGGATTCGGGACAACT
WI-13752a	106	T C A G T G T G A	CCTTCTCGTTA AGTGTCC	CCCTCCGTAAA AGTGTCC	AAGAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCTCGTTAAGTGTGGATATACCTTGGCTTGCAACCGACCTTTTACG GAGGATTCGGGACAACT
WI-14339	102	T G T T A C	CCCAATCAAA CAGTACATGA TTAC	TCCAGATTTCT GGAAACCG	AATCAATTAATGAATGTTCCAAACACACCCCTTCACTGGGTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACAGTACATGATTAG[T/G]CGGTTCCAGAAATCTGGATAC
WI-13744	115	C T A A A C T G A A	TGGTCTGAAC GATAAGCACA GC	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAAACACGTAAATGAACTTTCATGAGCTTTAGAT TTCTTTGCCAGCTAGGAGCTTGTATGGTGTGAACAAAACTGAA[C/J]GCTGTGCTTATCTTTC CTGATCT
WI-14061	68	C T ...		...	CCTTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACCTTAT [C/J]AACCAATTCATCCACCATTGTGTAATAATCTCATCTTCTGGGTCTGGATCTCAAAAAACAGAT
WI-15719	69	A C A T T C A G C	ACCTTTTCATC CATTACGC	TGATACTGGC AAGAGTTTAA ATT	TTACAGTTGGATTAACTACCACTACCACTGAATATACTGAATTAACCTTTCAACCCCTTTCATCCATTGAG C[A/C]AAATTTAAAACTCTTGCCCAAGTATCATGAACTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T C A A C T T	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAAT	TAATCCATCAATCTAAAAATCACACATACTAGATCAACAGAAAGTACCACAGTATGCTTTATTITGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAACTT[C/J]AGTTAGCAGCAAGCATCAGTCTTC
WI-15736a	27	G T C A C A	ATTTTATTAC ATTAAACTTG	GTCTTTGATA TGTTGGCTTAGT TTT	GGATTTTATTACATTTAACTTGCA[C/J]TTAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACAATAGAGATTGAATTTCTCAATAGCATTTGGAAGGTATTTTCCATAAATA TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGACACACAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACAACACAGTG
WI-13785d	72	G A ...		...	TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG AACMGTGCTAGTGACACATAGCTGTCAACAACACAGTG
WI-13785c	56	A C ...		...	



WI-13785b	40	C G ...	...	---	TCAAAACGACACTATAAAGTGCTTTAAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTCGGTAGTGACACATAGCTGTACACACACAGTG
WI-13785a	27	T C TGCT	AAACTGCAC ACTATAAAG	TGTTGTGACAG CTATGTGTAC T	TCAAAACGACACTATAAAGTGCTTT[C/J]AAAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGGTAGTGACACATAGCTGTACACACACAGTG
WI-13793	88	C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCAATAAAAATAGTTTTTACCCCCATTGATACACATAAAGGGATTT TACATTACAGCCTAGATATAG[C/G]AGTAACAAATCTCTCTGCCATAAATCTATGACTTG
WI-13794	52	A G TTCTTTCTC	TTCTCACCCCT TTCTTTCTC	AGATGGGCTC TTAACCTTGT	TAGTCTCTACAAATCCCTCAATCCATTTCTCTCTCACCCCTTTCTTTCTC[JAG]TACAAGGTTAAGA GCCCATTTCTTCAACAAACAAAACAAACATAGAGCAAT
WI-15729	35	A G GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCAATTAAGTGCACTTTTGAACCATGTGTAGACTGC[JAG]GGGCACCTTTAGAAAGAAAGCTGAGACTGAA AAGTCTGTCTTGACTTTCCAAAGGAAGGTAAGTCCCTGTTTGACGCCCGGGCTGCTCATTTGTTA
WI-13424	66	G A C	TGAGGTTTTTC ACCCTATTCTT	TTTTTCTCCC AGGGTCTA	GTCTTTGCACAAAGCTCCCAACTGGTTTGGAGTTTTCCTTCTGAGGTTTTTCCACCTATTCTTC[G/A] TAGACCTGGGAGAAAACACATGTGTAAAGTGGCTCAGGACATGAGGAGCCGCTTACAAAGAT GCTGGCTAAGGGCTTC
WI-14065	29	T C AATT	TCTTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAGGTCAGAGGCAATTT[C/J]AGATCCAGATTCAGCTTGTCTCATATAAAGAT TCAACTCAAGTAGCACAAATTTCTGTCTGCTTTTAACTCTGAACATCTTGAAGCAGCAA
WI-13446	22	G C TCACTCATCA	GCCATGTTCTT TCACTCATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACTCATCA[G/C]CCTCTGATTTTGATTCCTTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56	A C TGGGTGCC	TGAGCACATA TGGGTGCC	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGAAATGTACCTTACACATGGTGAGCACATATGGGTGCC[JAC]GCCCGAG ACAGCAGGATAAGTTTCAAAAACCTTGACCAGGAGGTTAGAACCAAGGCAITGGTTCAGGATG
WI-15702d	107	T C ...	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCTGTAAACAATACTAA[J/C]JGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T C ...	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]CTGTAAACAATACTAAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C T ...	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]CTGTAAACAATACTAAATGGGTTCTTTGAACAAATAGTTT TGA

48	G C A A G	A A C A A A A T A A A G G C T T T C A A	O C T A C C C C C T T T A C C C C	C A A A T G T T T A T A G A G A C T C C G A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G G T A A A G G G G T G A G G A A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T A A T G G G T T C T T T G A A C A A A T A G T T T T G A
113	T C			T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T T C C A C T G T A C C T C C G G G T A A G T T T C C T T C T C T G T A G A T [G/C] G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
56	G C			T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
3	62	G A		T G A T T G A G C T T A G A A G G A A G T C A T G T T G A A A T C A G A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
2	86	A G		C A C A T T T C A G C A A C A A T C G A G G T G C A A A C A G G G T T A T T T C A C A T T A A T A T A T A A C T G G A T T T T T T G T C A A A T A A T A G G G A [G] T T C T C T T T A A T A A C C A T C T C C T C A C T T C A T G G C C A G T
3	95	A G		A G G C T G T T T T G A G G C C T G A G G C C C C A C A C A T G A C A C A G T A A C C A T G T A A C C A T G T C A T G T G A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C C A C C T C C C A A C G C C T T T A C T T T C A G C C C T C T G C A
8	61	C T	A A G A A G T A A A T T A G G A A G A G C A A G A	A G A A C C G A G A C T C A A A G A C C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A A G G A C T T T A G A T G G T C A C G
3	47	C T	A G A C T T G A G A G C T T A A A A C A A C A C T	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T A A G G T C T T A C A A G G C C A A
5	31	A G	A A T A A A A C T T C C T A T T T C T T T T G C T T	T G C A T T T A T T T T C A T G T A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A A C A G A A C A G A G G C C T T T
3	121	G C	A A T A A A A C T T C C T A T T T C T T T T G C T T	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T C T A A A T T T T C A C C T T A T T G C T A A G T T A T A A A A T A A A A C T T C C A T T T T C T T T T G C T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
5	50	A G	A T C	T T G T T T T A T T T G G G G A A T G A A G G A G G G A G A T T T T A G A C T G A A T C [A/G] T T C T A G A G T A T T T G A C G A C T A C A G C T C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A C A G A A A T C C T C A T C T G G G T T G C C A G A C A G

79	102	C T C A C C	T C T A T T A A C A G G G T A T G T C A	A T C A T C T G T T T T G A G G T T G A C A	T T T A T G C T G T T G T T T C T A C T G G T G C T G C T C A C T A A T A T C C A A T C C T A G T A T G A T T T C T T T T A C T T G T G T C T A T T A A C A G G G T A T G T C A C A C C C C T T G T C A A C C T C A A A C A G A T G A T A C T T A A T A A A A C A A A G C A G A A A A C A C C C A C C A T T A A C A G A G G A C A C T G C A G A G G C T T A T G T A C A A C A C G T G C C G C G A G G C T G C G C A G G A C T G C A C T C A C T C C A A A T T C T T G G A G C A G A G
02	22	C A ...	C G C A G A G C T G C T G T A T T A A A	...	A C C G C A G A G C T G C T G T A T T A A A A G A C A A G C G T C T G C A G G G G C T G G A C C A G C T G C A G T G G G G C T C G G C A C T G C T G C T C C A G G A C T C T C C C A C C A C C C
37	24	A G A	A A A C T G A A A G G T A T T C C T C C	G C A G A G A T C C A G A C G C T T G T	T G A A A C T G A A A C G T A T T T C C T C C A A C A C G T A G A A A C T T A A A G C C G C A A A A G A A G A C T C A C A C C C A C C A C C T A G C G C G A A A A A G G A A G T T T C A G G T G A T A C A A G A T G T C C T G C C A T C A C A C C T G A A G G A T G G T
144	24	A C A		G G C C T T T A A G T T T C T A C G G T G	A T G T T T A T G A T C A A T T C C A A C A T A C A G T A C A G G A G G T G A A A T G A T A G A A A A A A A A A T C A T A T T A A G T C C C G T T A A C A C T A A G C C A G T A T T A T T C A A A A T G T T T C A A A A T A C T C A G C C A G A T C A C C A A G C T C A G T C A C T A C
24	92	A G ...	G G T T G A C C T G C A T A G A T T T T	...	G A C A A G A G G C A G T T T C T G T A G T T C A G C A G G C C A G A G A G T T A T C A G A A C G G T T G T T G A C C T G C A T A G A T T T T G A C G A C T A C T G T G C C A T G C C A T T C C T G T A A G T G A A A T T A A T G A A C A
25	88	C T	G C T T T C T C A C C A T G T C T T C A C A	G G A T G G C A T G G C C A C	G T T A T T T C T C A C A G T T C T G A G G T T A G A A G T C T G A G A T G A G A T A T C A C C A G C A T G G T T A G G T T C T G G T G A G G A C T C T C T G G C T T A C A G C T G G C T G C T T T C T C A C C A T G T C T T C A C A T G A G C C A A A G A G A C A G A A C A A G C T C T C T G G T
36	120	G A	T G T T G G C A C C A G A A A G C T	C A G T A T G T A C A G T G A C A T A A C A	T T G T T G T G G C A C C A G A A A A G C T C T A T G T T C T A T G T T A T G T C A C T G T A C A T A C T G T A A A C A A G A C T G C A T T A A T A T T G T T T C T A T A G A T T G T T T C A A T G
138	23	C T	T C C T T C A G T A G T A G T A T A T T C A	G C T C A T T T C T T T T A G T G C T A A G	G G C A G G T T A T T C A T A A T T T T C A A A C T T G G A A G C A A C C A A G A T G T C C T T C A G T A G T A T A T T C A G A C A A T C G A A A T A T T A C T T A G C A C T A A A A G A A A T A G C T A T C A A G T C A T G A A A A G A C A T G C A G G A A C C T T A A A T G G A T A T T A C T
351	74	G A	G A C A A T C	T A A T A T T	T T T T T A A G A G T G C C T T C A C A T A T T A T A T T G A T T G C A C A C A A A C T T T T T A A C T C C T C T G T C A A A A C A C A A G A A C A G A T G A A T A A G G A A G C C C A G T G C T T T T G A G A T A G A A G C C T T C T T C A G A A T C A C C T C C
b	59	C T ...		...	T T T T T A A G A G T G C C T T C A C A T A T T A T A T T G A T T G A T T G A T T G C A C A C A A A C T T T T T A A C T C C G T C A A A A C A C A A G A A C A G A T G A A T A A G G A A G C C C A G T G C T T T T G A G A T A G A A G C C T T C T T C A G A A T C A C C T C C
a	26	T G A T	T T T T A A G A G T G T C C T T C A C A T C	T C A T C T G T T C T T G T T G T T T T G	T T T T T A A G A G T G C C T T C A C A T A T T A T A T T G A T T G A T T G A T T G C A C A C A A A C T T T T T A A C T C C G T C A A A A C A C A A G A A C A G A T G A A T A A G G A A G C C C A G T G C T T T T G A G A T A G A A G C C T T C T T C A G A A T C A C C T C C

31	82	G A	---	---	TGAATCAATGGACAGTTTGCCTCTGTTTGTAGTGAACCCCTCACAAAGCACTCTGCATAGTCCGCTTTCTGCTCTTTAAAC[G/A]TGCCTGGTTCCCTCTGCCAAACITTTAGGATTGGCCCTCCTCAGGGCCCTTGTCCCTGA
3	24	A G	---	---	ATCACCAACCGTGTCTAAGAACAAAC[A/G]TCTTCATGTCCAACTCATATCCCCGGGACTTTGTCAACTGCAGTACACTTCTCTGCATTGAACCTGGCTTCTCTGGAGGGAAAGCTCTCTAGAGGCCAGGTAAGGGGGTGCAGCAGTGGGGGTATATCTGGGCTGGCCAGTTGGAACCCACGGAG
34	99	T A	CTGCTGTC	GACTTCTCCAC	CAGAAACCTCTTCTGTGTATTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGAGGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT[A/G]CAAGAGGGTGGAGAAGTCTTGGCAAG
75	103	G A	GGCAG	CCCTTCTTTC	CAGCTAAAGGATCACCTGCAGCTAAATACAGATAGAGAAAGCAACAAGCCAGGCAAAATACCCATCAGAGACAGTGACAAGAGCAGCTGGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGAGGGGAGGAGCCT
79	96	G A	TGGAGGTCA	TGTAGATGC	TAATTTAAAAACACGCGCTTCCACATAGTGGTGAGGCGATCTGCACATTTTCTCTAGAAGGACATGATAGTGATGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCATTCGAGGGAGGAACAG
31	49	C G	ATTGT	CTTATT	CACAAATAGTGAAATTATCTGAGCAAGAATCATTCTCATTTAAAAATTGTC[G/A]AAATAAGTCAGAAAGAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
36	105	T A	---	---	AATGGGACTTTCAACAAGGGTTTAAACTAATCTAATACAACTTCTACAACACATTCACAGAGCATATAACAAGAATTATTTACAGGCAGCTAATGTATTAAT[A/A]ACCATGAAAAAGAAAAAATTTG
73	31	C T	---	---	ATCTAGATGTCAGCAAAATGGGCTGAGACTGT[C/T]TGTCTGTAGATGACAGTGTGTATGTTTCTACTCTATTACAAAAATTAAACAGAAATATGGCTTCGCTTTGTGCAAAATGTTTATATCACAGTC
37	103	A C	AAATAAAAA	TG	AATTTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAAAGATAAAATATGTCATTACAGCAGTCATTTAAAAATAAAAGACTACAGATACAAGGAAATAAAAA[A/C]CACITTTAGGAGATGAAAACACAAAA
38	60	T A	G	TTACTTT	TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTGT[A/AAA]GTAACAAAATGAGTTTACACAATAAATAATTAACACATACTTATGGGATTTGTTGAATGA
33	47	C G	---	---	TTTTGTGTTAAGAACACAGCATTTTGAATAAACCCTATCTGCCCATG[C/G]TTTACAGCCCTTTTAAATTTGTAATATTTATATAGTCGTTTATGGTACATATTGATTGTC
	63	C T	CGTCT	CAC	TTAGAAAACTGATAAAAGCAACACAACTTTTGGGAAAGCACCACTGGCAGCTCCTTTGTGCTA[C/T]GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
15	22	G A	---	---	ACATGGCAGATACAGAGCTGT[C/G]ATCTTGAAGACCACCACTGAACAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGITTTCTGACCGCTCTGGAGCGTTGAAGGGTGACCCAGCACATTTGCACATGCAAAA

102	59	T C A G A A T T C	GATAACATAA AATGATCATG	GCCATCTCTC TTTGACTTTT	CCAAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA/T/C/GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
3	101	A G A	CCCCTTGAAC TCAAGTCATC	AAACTAAAC CTTTGTGCCTA AAA	GTGGAAATTTTATTAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAGATAACACAT CTTCTTGCTCATCCACTTTGAACCTCAAGTCATCA/G/JTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTTAACCA
159	73	T C G T G G G	GCCTTTGACTT	TCCACACTGC OCCC	TGAGTTACAACAAATGAGCAACAGTTAGAAAAATTTGTTTTATTCAAACTTCCTAGCGTTTGACTT GTGCGG/T/C/GTACTCAAATGGGGGCGAGTGTGGACGGGAGGATTGCAACAGAGTTCATACTG CAA
335	50	A T T A T	CTAGGAGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTACGGTGGTACTAGGAGGTTGAGGTGTAGATAT/T/C/TTCCCTCTCTCTC GTGAGCCCTTACTGAAGACAGGATGCCCTTCTGTGTTTATCAGCTGAGAAAGGCGAGTCTCGCCATC TTAAAGACCTGCCCTCC
a	112	G A G G G A A	AAAGGCACAC	CTCAGCCTGOC TTGACC	TTCCATTTCATTATGCTTGGCTTTACCAATTTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGGTCAGAAAGGCACACACGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
340	18	T C	---	---	ACACAATATAATTTCCATT/T/C/JCGAGTGATTAAACCTATTGTTGTTTAGAACCAAAACAAACTAC AAGAAACATTTTCAAAACCTTTTTTTTCAGGCTGA
308	52	T A C T A C C C T G T	ACCCACCACA CTAOCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACCTTTAAGCAACAGTTAAAAAGTACCCACACACTACCCTGTT/A/AAAACTTTAAC ATTGTGATGCCCTCTGCATCAATTTTGAAGAAACAAAGAAAAACACAACTGAAGGCCCCCATGTA AGTTAAAAAAATCGAGTCAGCATTTATT/T/AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
816	29	A T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/T/TTAGGTGATTGATACAAATACGATCCATAA
'c	71	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT/G/T/GTAGGTGATTGATACAAATACGATCCATAA
'b	70	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT/G/T/GTAGGTGATTGATACAAATACGATCCATAA
a	45	C T T T T A A A	GCTATTAGGC AAACTGAACA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATCATGGTAGGTGATTGATACAAATACGATCCATAA
173	57	C T C A A A A A	GGATACAGCA GTAAAGAATA	CCACTCTAGA ATGTATGCTCT	CACCTAAATCATCTAGAAACTGGGATACAGCAGTAAAGAATACAAAAATCCTGC/T/CTTTATA GAGCATACATTCTAGAGGTGGGAAAGAGGCAATAAATA

836	28 T C ---			TCCTTGGAGGGATAGAGGACAGAGTGTTCGTTGATTTTGGTTTGGTTTGGTTGTCATT GGTTTTGTTTTTGGCTAATTTGCCCCACCCTATAAAAGCAGTGCCACCAGAGGCAG
856	60 A T A A	TGGTGACACG GAAAATACTT	TTTGTTTGCTA CTTTTACAAA CTTT	ACATTTCCCTTATGATAGCAACAACATAATATGATGGATGGTGACACGGAAAAATACTTTAATATTTAA AGTTTGTAAAAGTAGCAACAACAAAATGAGTATATACTATATAAGTGATAGAGGATGATATGAAAAA GGCTATAAAAAGCTCCAAA
863	61 G A ---		---	ATGGCAATTTACTTTATAGCAATGAACAATAATTTGTCAAAGGGCAATAATTTTGTCTGIG/AJAG TTAATAAAGTTAATAATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGCCACT ACCTGGC
867	46 T C A	GACATTCCAA GGCTCTCTAAC	TGGGGCTGCAG ACACTC	TTTTAATTAAACGTAAAAAGGAGGACATTTCCAAGGCTCTCTAAACA/TTCGAGTGTCTGCAGCCCCA TTCCGTTTGAGATGTGAATGTGTAAACCCAGGGTGA
733	98 G A A	CCAAATTGAC AGATAATCTGC	GATGAGGTCAG GCCATTTATT	ACGGAGTCGTCTCTGATGTATTCTTGTCAAAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAAATT AGAAAAAATCCAAATTGACAGATAATCTGCA/G/AJAATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
lb	79 A C ---		---	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/NCJAGGTGCCACTAAGG ACTTCTCCAT/CAJAGCTGCCCTGTGTGCACGTTGCCCTGGCTTTGCTAACCCCTGGTGTGCATCT GCCGTGTCTGTCTT
a	50 A C C A	CATGTACAGG AAGAGTTGTCT	AAGTTTTCCTT AGTGGCACCT	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/NCJAGGTGCCACTAAGG AAACTTCTCCATAAAGCTGCCCTGTGTGCACGTTGCCCTGGCTTTGCTAACCCCTGGTGTGCATC TGCCGTGTCTGTCTT
907	48 G A G G A C T G A C	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/G/AJATCCCCTTGGCAGCAG ACATTTGTGAAGCTGCTGTGCGGCACACCCCAATCAATCAGTACTCTGCACTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
911	52 G A C	CCAATACATT CAGTTCCTGGT	CAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCACTTCTCTGGT(G/A)AAGGTCCCTTTTC CTGGTTGCAGACAGATACCTTGTGTATCCTCACATGGCAGAGAAAGAGGAAAGTAATCT
913	88 C A ---		---	CTGATGCTTTGACATCTGGGCAATGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGCCAAATTC TAGTGATAGTAGAGGACTCA(C/A)CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAAC CTACACCTCCAACCACCT
914	66 G C A	CTGGACACAG TTTTCTTAGC	CAAGCCCAGGA CAATAAATTC	ATTTCCTTGATTGGCTGTCTGAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTTTCTCTAGCA/G GJGAATTTATTGTCTCTGGCTGTGATGGCTTTTCACAGC
926	49 T C ---		---	GTTTATTTTCAAAATGACACATCCAGATTGAAATGGGCACCTTAGCGAAT/CJACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAGACAGTTTTTCAATAAAAAATTTTCTTAAATCAGGTCCA

33		ATGTTTAAACA	TGGAAGAAGATT	GCATCTTTATTACCACAGAACTCATTTTATGTCCCTTAATCATTTGTTTAAATATATATATAAGCATGTT
89	C T	CAACATATC	CCAGCC	TAACACAAACATATCAAGGAT[C/T]GGGCTGGAACTCTTTTCCATTCTATAGAAAAGCACTAACCATC
		AAGGAT		CATTAAAGCAG
30		GGAGGAGTCC	CACAACCAACC	CAGTTCTGTGTTCTGGAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG
55	C T	CTCATGGAT	AATACCGC	GTGGTTGTGGTGAATTTGGGGAGCACGAGGGAGAGCAA
16			---	TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCAGACATAACA[T/C]CTCTAAATCATCCTCTA
47	T C	---		GATCAGGGAGTCATAAGGACCATTAAGGCTCATTACACACAGTACTTTATGGAAAGGATT
			---	ACATTAAACAGCACAAATTAAGGGTCCCAACGAGGTGGTAGTGCCTTCCACTATGTGAGGACAC
80	A G	---		TAAGAAGATGGT[C/A/G]CTATGAACCAAGCTGCCGGTGCATGCTCTTAAACCTCTCAGC
			---	ACATTAAACAGCACAAATTAAGGGTCCCAACGAGGTGGTAGTGCCTTCCACTATGTGAGGAGGA
32	C T	CACAAATTA	GGAGGCACTA	CACCTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
		GGGGTCCCAA	CCAACCTC	
48		AGGAAACTG	GATGATCTTAC	GAATAAAGTCTTATTGCCGTCTCTCAGGGAAACAGGAAACTGCTAACTTGTACG[T/C]TCCAACA
56	T C G	CTAACTTGTCA	ATCAGTTGTTG	ACTGATGTAAGATCATCTCTGACCATTAGCGAACCTGTAAAGGCTTGCTGTTCCCTCCAGCTGA
		G	GA	
		CAAAAAGCTA	ACAGGAATGTC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[A/G]GTAATATACTG
52	A G	TTTTCTACAC	AGAAAACAGT	TTTCTGACATCTCTGTTATCAACTCTCTCTGAAAATC
		TTGA	ATATTAC	
		AATAATTTAT	AATGCATTCAT	GTGATTGATCTGTAATTTATGGGATTTATTTCAACTCTAAAATTCGAAGTGAATAATTTATCT
		CTCTTCTTTT	TTGGGTTTT	CTTCTTTTCAAGGG[A/G]AAAAACCCCAATGAATGCATTTTCAGTTTCTCCAGGCCTTTGAACCTGC
58	A G	CAAGGG		AGCAGAAAAATTCAGGA
			TCAAACATAAT	TATTTTTTAATTGGTTGATTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTAGTTTGAGGAG
		GTGATTTGCT	CTTCCATTCTA	GGGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAGAAGATGCCCCATCTCACACCTGGAG
176	C T	TCGTTCAAAG	AGC	ACGTCCATGAGCACCTCG
		TCAGTGGTGT	CACCTCTGACA	TAATTGATTCAGTGGTGTATTGGATTTT[G/T]TTATGCTAAGTATATGTCAGAGGTGGAGAAT
		TATTGGATTT	TAATACTTAGC	AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTGTGCACAGGAAGTTTTTGA
181	G T	T	ATAAA	GAGCTCACAAA
		TGCATTAAAT	GCTATGTGCTC	TGATTACATTTTTTAAATATCGCTTACCAGGCCCATCTAAGCCAAATTCAAACACCACTCTGCATT
192	C T	GAAGCTGCAG	AGCTTTCCT	AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCCACTGATCGGAAAGAAACGTA
			---	AAATCTCTCTTTCACACACAGATGAACITTTAATAATTACAATGCACCTGAAAATGCCCTTCTTGA
102	T A	---		TTTCC[T/A]TTCAGTTTAGGCCTCAATGGGCTCTCTCCTCAAGGCTGGACCTCAAAAGGCCCAAGTT
		GACAGAAAAA	GTTCCTAGTTC	
		GACTCAGACT	TGCACAAACTT	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAACAGATGGATAGACAG
100	G A	GTCTAA	CA	AAAAAGACTCAGACTGTCTAAGT[A/G]ATGAAGTTTGTGCAGAACTAGAAAACAAAATCCACCT

23	68	GA	CA	CAATACCTT CATGTACCTAT TTCCTACCTG	CACTGGACATA TTCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACAAATACITTCATGTACCTATGAATAA G/AJACAGGTAGGGAATATGTCCAGTGCACAAACAGAGGACTCACACCTGTGTCATAGACAGCACC
33	91	A	T	AAGGACGAT TAGTATCTAA TAAACA	GGCATGTCCA GTGTTTT	CATAAGTTGCATTTATTCACGTCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA/A/TJCAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAACTAC
70	100	CA	T	CCTGCCCTTAT ATTGGAATTC T	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTTAGCACCTGAAATTTAGGCAAGAGAAACAATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCCCTTATATTTGGAATTTCTA/C/AJAGAGACCCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
2	38	T	A	CA	TGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAATCA/T/AJCTACAATACCATATACAACATACT TTCAATCACAACTCAAAATATAAAATAACCTACAAAATCACATTGC
2	40	A	C	TCTATG	TAT	TGGGATACCCCTTTTACTTTGTTGTCTATTTTATCTATTG/A/CJATTATAAGAAAAGTGTGAGACCTT ATGGCTCTGCTTATGGGCAATATGCAATATAATTTGTGTTGTTAAATTTAIGCAT
33	35	C	T	A	AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA/C/JATTGTAAGTTAATGTAAATGGCAGCAT GCCAAAGTTTAAAGAGGACTATTTCTTTAAACAAAGACAGTGTCTGACATTTATTTTCAAGT
33	88	T	A	TC	AGCA	TTTTTTTATTTGCAATTTGAGTCTTTTATTATATTGGGAATTTGCAGTGATTAACATTTGTACAAT GCACAAAATCTGTCTCTCTC/T/AJTGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTTGTCAT
7	58	T	C	GATTTT	AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATAGAGATAGATTTTTTCTGATATACATTT/CJCATCTT ATTCACCACGAGCACACCACACAGTAGAACAGTTCCACACCTGATAAATTCACAAGATG
2	17	GA	...	...	...	GCAGAACCAATTAAATG/AJAATCTGCAAGTTTTCCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGATAAAGGACTGCTTGATGTGACAGTCACTGGT
9	81	T	C	...	...	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTTTCCAGTATCATGTAC GCACATAAAAAA/T/CJGTGTGCTGCTGCTGTGAGTGAACCATTTGCTTAAAGATAAA
6	97	A	C	CCAGAGTCGC	TTTGAAGAGA	ATCTGGTATTTGTGTATCCCAACAAGTATACAGAACTACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCAGAGTCGC/A/CJCTCTCTCAAAATGACACACAATTAAGACG
2	59	G	T	ATGT	TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATAATAATACAGCTTTTTTTCATTGAAGCTTTT[G/T]TACCT TACTATCTCTAGGCTATTTGGAGTGTCCCCAC





82	49	A	GCACACCAG	GCATGGGTAA	GAGACTGCCCTGTGACACAACTAGCTAGCTGCACAACACCGGGGCAAAATATC/AT/GCTGGATTAAACCC
			GGCAAAATA	TCAGCA	ATGCTAATGGGTACCCTTATTATTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
98	38	T	GGGOCCTGGC	ACTTATCCGTC	GTGGACCTCTACAAGTACCATGGGCCCTTGGCACTATGTC/CTACTCTCCCTGACCGATAAGTTGGC
			ACTATG	AGGCAGAGTAG	ATATGGTTCAGATTGCTGTCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
01	42	T	CATTATTGAG	GTGTAGCTT	TCAAAGTGGTAAATAGCCATTATTAGTATTCCTTGTCTTGTGATTC/GTCTACGTAAAGCATGTAAAGACT
			TATCTTGCTT	ACATGCTTACG	ACAACATTACGACCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAAAACAATTTTGTCATTCAGAT
			CTGAT	TAGAC	T
			TGGCAAAATA		
10	104	A	TGCAATACAA	TTGAAATGGT	ATGTTGAGAGTAATAATGCCCTACATAATTTAGTGTAGTACACCCCAAGATATTTTTGGGGAGAAGAG
			TAA	TAAACTGGCA	TTGTTGCTTTTGTGGCAAAATATGCATAACAAAAATATTTGGCAGTTTAAACCATTTTCAAGAGT
			CATTTGCAAT		CAGTGTGATGACATTTCAATTGGGAAAAAGATTGTGCAATTTGCAATAAACACCATCATTC/CJCTGAG
			AAACACCATC	GGACCTTATCT	TCCACAGATAAGGTCCCGGAGAAAGGGCTTCCCTCTCTTCTCGCTGGGTGACGTTCCACGCGAGT
39	57	T	CA	GTGGACTCAG	GAAGCCCTTCTGGAATG
			GCATCATATG	GGACAAATTGT	
34	52	T	AACTGTCTAGC	AAACATAGCT	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACGTGTCTAGCAGTATTATTC/GCTATTAGCTA
			AGT	AATAGC	TGTTTACAAATTTGTCTGAAGGGGTCTAGATGTGTACACCCCAAGAGTGGTGAATTCCTGA
99	34	T	GGGCTTGACAC	GGAAAGCCAG	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTTC/CTTGTAAAAATCTCTGGCTTCTCTGGCTGG
			AAAGTTCTAA	AGATTTTAAAC	TGAGGAGGCACAGGCTGGGCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCCTCCACTCCCCAG
				AA	CCCACATCTTGGCTCT
59	28	T	AAGACACCGT	COCTCTCCTCA	CTGTCCGGGAAGACACCGTGCAAAATGC/CTAAAGTGCACCTGAGGAGAGGGGAGGCTCTGTGACTC
			GCAAATGC	GTGCACTTT	CCAAACCTCGAATAATTTATGAATCTAAGAGTCCAGACGAGTTTCATCCACGGAGATCTGC
				TTGCTACTAAA	
48	41	A	CCTAGTGGCAT	AGTGACATCC	TCCCCAGATTGTATGGAATGCCCTAGTGGCATTAAAGGATGC/AG/GTAGGATGTCCACTTTTAGTAGC
			TAAGGATGC	T	AACCGATGTTAATTCACTACTCCATGTTAGGTGCTTACTTGGATTATCTCACITTAACCAACCACA
34	64	T	CATGCTGTAA	GGAAACAACA	ATGAGAGGTAAAGTGTCAACAGTAGGCTTAAATATTTCAGTAAACCATGCTGTAAACAGCTGTGC/G/
			TACAGCTGTGC	AGCCTAAATGG	TJCCATTTAGGCCTTGTGTCTCCATTAGAGAGCAGGAGGAGGAAATTTAGCATAATCTT
			AAAGGATGAA		TTTATAAGCTGAATGAAGAGGTGACACAGCGGACACTGTCATAAGTGGAAACAAAGGATGAAGCT
30	75	A	GCTAATCATG	TCCTCCAGGG	AATCATGGA/GA/GCAAGCTCCCTGGAGAGACAGGGGACAAAAATCAAGAATGAGCTGGAGAAATTAA
			GA	AGCTTGC	TOCTG
			CATGTGGCTGG	CCCTCCACCAT	AAGGTTAATGGACTCACAGTTCATGTGGCTGGGAGGC/CTCACAAATCATGGTGGAGGGCAAAA
5	39	T	CAGGC	GATTGTGA	GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
			AGTTGGCATTC		TATTTGAGTATTCATCCATGGGCTTCTCACTCCCTATACATTCACGGGTGAGGTAGTCTACCC
16	123	T	AATAGCCTAT	TGAAACTCCCA	CCATAGGTTTCAGAACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATC/CTTAACTCCATGT
			C	CATGGAGTT	GGGAGTTTCAATAATA



		GACTGCTAAG GATTTAAATTTG TTAAAA	TGAAGTGTAG ATGGCTAAGTA TTAAAA	AAGAGAACAAATTAGTCTAGTCCAAACATGATTGGCAGTTGGCATAATCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTTAATTTGGATJAGJATTTTAACTAGCTAGCCATCTAACACCTTCAAGCATAAC
91 A G		CACATGGCAA TGATAATAAA CA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGTATGTCTCTACAAATACATTTCTCAAACCTCAAACATCATGCTTGAATATCACTGAACCTT GTCACCAAGAAGTACATGGCAATGATAATAAGAAATJATJATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGATAAAACAATGGAAATTTGGAAAAAATAGGAGTAA
105 T A		GAAA		CATATGCTGCTTTATTTCTGTAGGATACACTGAACCTTATAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTTAACCACTCCTACAAGAAATGTTAGTATGTTATGCTATTACATGTTT ACTTTTGATATTGTCTCATTATCTATGTJATJATATAATAATGTAAGTACAGTAAGTAGGTGATCC TGCAITTCAGGTAAAGCGGTAGGTGGAAATCCAGATTCTCTCTTGAGGAAAA
164 C T		---	---	CGGTTAAGAAATACCTTTAAATTTAGGTAATAAAGCTCAAGGAGGTGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCCCTGGCTGTCAGTGTGCTCCAGGGCTTGACAAGCAGCTCATTCAAGJCTJ GGCCCCACCATGGCCCTAGGGTGTCAACAAGTCCAGGCAATCATGGCTTCTCGTATATCTGATCC AC
131 C T		---	---	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACCTCTGTTTGTGTTTATGCTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTTGTGGTATTTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTGGAAAAAAGCTTCTCAAATTTGJATJATCCAGACTTCAGGAAAAATGATT TCCACATGGTAAGGCCAGAGTCTCCAGTGTGGTCCATCCAGAAGCAGCTTG
175 G A		---	---	CTTGATTTAATCAGGGCTTGGGGTATAGGGGATTAGTCACTGTCAAGTCATAATAATGCATTTA TTCAGGGAAAACTTTAAJCTJCTCTTTGTTCTCTCCAAAACAGCTGCTGGAAACACCTCAAATTA GGGATGTTTCATCTAAACACCTTTTACTGAACTTGTATTCCTTGGCCAGAGGAGGCTTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTCGGGCAATAAATGAATACTTGATGCATTCATACAGGCAAGAA TCCCAGCATCCAGAGAAGCTGTGTGCTGJAGJCTGCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCAAGTTCTAGTCTGCGCTCCTCGATTTCCCTGCCAGCAGTCTTCTCTCTCTCTCTCTCTGCGCC
96 G A		CCCAGAGAAAG CTCTGTCTGC	CAGCCATGGCT TTGCAG	CTCTG
b 193 C T		---	---	ATGCTTTTGCAATGATTTCTAATATTGCCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGGTGCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTGTJCTJCTGGTT CTTCCCTTTACATCTTTTGGGGGA
187 T C		---	---	ATGCTTTTGCAATGATTTCTAATATTGCCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGGTGCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTJCTJCTGGTT CTTCCCTTTACATCTTTTGGGGGA

		GGTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAGAGTATCTTTTACAAAAAAGGTTAGATAAAGATCTC ACATTTGTAAGGCACATATGAACATTTTATAGCAAGCACAAAGGGCAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[TA]GCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
b	112	T A ---	---	TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[AT]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
a	73	A T ---	---	CTAATAATCCTGGGCACATGGATCCAAAGAGAGATTTTCAGCAGATTTTATTATAGTTACTTAA CAGCTAAATAAAGGGTGTATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[GT]ATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
i	165	G T GCTG	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGGACGTCCTGGTAGTCTCTCTTTTACACAACTTTCCCTGAGA ACTGTCCAGTCAAGTGGACCTTCAACAACACGAAACAGCTAAAACTCTGAGAGAAAAAC[CG]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
b	68	C T ---	---	ATTGTAATTAATAATTTACATGGGCCTATTATTAAAGGACATTGTAATGTTCCACTTTGTTTAA [CT]AATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAAGTTTGAAAAATGGCGG
la	42	G C ---	---	ATTGTAATTAATAATTTACATGGGCCTATTATTAAAGGACATTG[CG]TGAATGTTCCACTTTGTTTT AAACAATTTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAAGTTTGAAAAATGGCGG AACCAACAAACTAAGAAATGGGAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTCATA[TC]AGCAATGGATGCTGTGTGAGAACATACTGCCAATAAACTTTAAAGAAAAAGGA ACTCAATGAAGTTACTGTATATAAAACAGGAGCTCACAGCAGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCCAAAAC
p	75	T C GTCATA	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTAAATCAATCAATCAAACTCCAGCTGTTTCTCTGCTTT TTACTTAGCAAAAGGAAACTTTAGTGAATGCTACTTGACAAGAAAGTCAATTTCTCAAGCACAI T[CG]ACCCAACTTGAAGGTGATTGAACCCCAATAATGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGGTTATATTGATGTTGCCAAT
i	134	T C ---	---	TGCTAAACACCACCATTTAAGGAGAGTACTAGGAAAACTACCAACACACAGCATGTGAAACAGT TGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGC[CT]GGCTAATACACTGCAATATTTA TGTTTAGCAATATTAGCTGTCTGTGTATACCAGAGAGCGGTATCTGG
jb	106	C T AGCACAGC	ACATAAAATA TTGCAGTGTAT TAGCC	

10a	28	T C A G A G	A A C A C C A C C A T T A T T A A G G	G C T G T G T T G G T A G T T T T C C T	T G C T A A C A C C A C C A T T A T T A A G G A G A G T C J A C T A G G A A A A A C T A C C A A C A C A G C A T G T G A A A C A G T T G G C A C G G T G T A A A G G G C A C A G A C T C T G G A G C C A G C C G G T A A T A C A C T G C A A T A T T T A T G T T A G C A A T T A A C T G G T C T G T A T A C C A G A A G C G G T A T C T G G
70	53	A G A A C A T C A C A	C A A C C C C A A A A C A T C A C A	G C T T T T G G A G T G T A T A A T A G T A	G A T G T T A A T G A C A C A G A T C T C C C A A G T A A T C C A A A C C C A A A C A C A T C A C A J A G J A A T T A T T C A T A C T A T T A T A C A C T C C A A A G C A A A T A C T T C A A C T G C A A T C C
36	151	A G A	G C A T T C T T C C A A A A C A A A G A	C C T T G T A A G T G A C T A T T C C A A T	A T T C T G T A G G C A A A G G T C A G A A A T C A G C T A G C A C T A T A T C T T G A C C A A T G G G T A G T C A G C C T C A T C A C A G A G A T T T T T T T A A T T A G A T G A A T T T C A C A T T T A A A A C A T G G T A A C T C C A A G C A T T C T T C C A A A C A A A G A A T J A G J A C A T T G G A A T A G T C A C T T A C A A G G A C
31	32	C A G	G A T C T A A C A G C T G C A G A A T G	A A A A G C T G G G A A G G A A G A G	C C T G A G G C A G A T C T A A C A G C T G C A G A A T G G J C J A C T T C T C C T T C C A G C T T T T G T G A C A A A A C A A T T C T C T A A G G C A T C A G A A G C A C T G A G T G C A A A T G G T T G T T C A G G T A C A A G G T C T C
14	225	T C		---	T A A A T A C T G C C A A C T A G C A T T A C G T C C A C T C T T G C A T C A T T A A A C A A A G G G T A T T T C C T C C T T G G T A T T T C A A A T G A T G C A T T A T A C A A T A A A C G A A G T T A G A A C T T A A A T G C A C C C T G A T T A A T A T G T A A A C T G G T A A T T T G T T T A A A A G C A T A A T A A T T G G T T C C T T C T T C A T A A A A T G G A A T T T A A A T A T T C T C T G A T A G C T T G A G G T J C J A T C A T T A G T A G T G C A A A G T G T G
24	112	A G		---	C G G T T T G C T A C A C T T A A T G G G T T T T T T A A G G A T T T T T T C A G G T C T T G T C A G C A A C A T C A A A C A A A G G T A C T G A G T A C C A G G G T A C A G A G T G C T G C C A J A G J C A C C T T A G A A A A A T T A C A T G A C A C G A G A A A A T G C G C T C T T G C T C T G A A G A G C T T A C A G C T A G G G A T T T G A C A A C T C A C A G T C T T A G G A A C T G G G C A A G T A A G G C A A T T C T C A T C C C C T A G A G C T A T T G T G
39	139	T C A A T T C	G A A A A A T G A G A T G C A G T T A A	T C A C T T T G T G G C T T T A A T T A T	G T A C A A A A A A G C T G A G A A G C C A C A C A T G G A A G T G T C A A G A A A A C A T T C T G A T A G G T A C G G A C A A A A G A G C T C C T T C A A T C A A A G G A G T T A C A T A T T A G T T C T C A C C A T G C T A G A A A A A T G A G A T G C A G T T A A A A T T C T J A G A A T A A T T A A A G C C A C A A A G I G A A A C T G T T G T T C T G G G C C C T A T G T T G T A G A T T C T C T
11	216	T C		---	T C C C C A G C T A T A T T A T T T G G C A C A G A G T G G G C A C T C A A A T A T C T G A T G A A C T T G A A C T G A A A A G A G G T C C C T T A A C A A G A T A T C A T C T C C G A A G A G A A G T C C C A C C A T A T A A A T G A T G A T C A A G T C C A G A A A A C T T T G C C T T C C C A A G G A A T G T T T C A A T T G G T T C A A A G C A C A C T G G T T C C C A C T T T A C C A C T T J C J A T G A C A T T G G A C A A T A G T A C T A C T T T T C T A C
13	112	G C		---	G C C A G T C T C T A G T A A G T C T A G G A C A T G A C C A G A A G C C C T G T T C T A T A T A G A G A C A A A C A G G T G G C C A T A C T T G G T G A G G A T A C C G C T A T T C C C A G A T J C J A A G A T T T G T G G A A G G A G A C C A T G A C A G A T G A C A A C G G A A C A G T T T C T C A A A A C A G A G G T A T G A
57	74	C T		---	A A A G C T T T A A A A A A A A G T G G T G C T A T C T T A G A A A C A C T T T C A G C A A G A T C A A G T A G C C C A G C T A C A G C C T J C J G G T G C A T C T T A A C C C C T C C C T T T

7	37	G T	...	...	...	TGCTCTTTTATTTCACGTTTCACAACACACGCCGTG[G/T]GGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGCGGGAAGGTCATCTGTTCTGCTCTATGGACTGATTGAATTTGGATGGCCAG CTCCAGAAATGTTCCACGTGGGGCAGCTCTGTGGGACAGAGGCTGAGCCCTTGCCACACTGGCAOCCA AAGAGGTTGCACGATGCAGCTTGCAGTGGGTCCAAAGCCGGGTGCTGTG
7	121	T G	...	...	...	AATGCTGGAGAAACATCAACATTGAGTTGACATTGTTTGGTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAATAAAGT[G/J]ATAATCTT TGATTAATAATAATGTTTATAAATGTTTATGAAGCTCAATACATTATCTTTTAAAGTAAGTAAAA TTTTAGAACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTGGAG
114	G C	GCTGGGA		CCTCCCAAGTA	AAAAATTAAC CAGGTGTGGTG T	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATG[G/C]ACACCCACACCTGGTTAA TTTTTTAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAAACCAACTAAC CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT[G/C]ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCCACACCTGGTTA ATTTTTTAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAAACCAACTAA C
1	51	G	...	...	...	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[CT/CT]TTTTCCATAATAACACAAAAATTTCTAAATATCCTTAAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAAATTTTTTAATTGAGGGAATAGGCCAAT TT
12	71	C T	AGCTTTT	TACAGACTTA	TTAGAAATTTT GTGTATTATAT GGAAAAAG	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[C/A]AACAGCATCAGTAGGTACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAACGTGTTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
188	36	C A	CTCAGTACAA	TGGTACGTGCT	CAAGTGTA CTACTGATGCT GTTT	TGCTATTTCATGACAGACACGTCGAGACAAATATCTTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAAACCCCTGAGACTTTA[G/A]ATCTGCAAGGGGTTTAATAAT GCAAATATCACAATATTTCCATTTTAAACACCATATTTAAGTTTTCCATTTTCTTAATAGAAAAATGA TAAAAAATGTTTCCCCCAATAT
a	108	G A	CTTT	CTAATAGTGG	CATTATTAAAC CCCTTTCAGA	TGTATAAAAAATCCAACTTGTTCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[G/G]TACAAAAAACAGCAATTTCCCTATGGCCAGTGTCTACAGAAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCAGGATGAGGCCAGAACCA AGTGTGTC
337	87	A G	AAAGTCCA	CCATATACAT	GCATAGGAA ATGCTGTTTT	AGTGTGTC





		GCATGCTGTG TTACTCTATTT TGTTTC	AAATGCCACAG GTGGCT	AAACACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTTGTTC/TAAGCCACCTGTGGCATTTT CAAAATATGATAATCTCTGCCACCATCTGCTTTAAACACAAATAGAAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAGGCTACCATCAGTACCTTAGCACATTATAAAAAATAAAACCAAC ACTGCCCA
46	C T T	ATCACAGCAG AGTACCTTTCT T	CTTCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACTTC/ATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTGGTATAATGACCTGTGTCAGTTAATCCA
29	T C AACT			TCACTTATCTCTTTTGTGGTGAGAACCTTAAATCTAAGAATGATCAATTTCAAAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTTCATTGACTCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
b	112 T A ...		---	TCACTTATCTCTTTTGTGGTGAGAACCTTAAATCTAAGAATGATCAATTTCAAAATAAAGATGG TAGTGAGC/TTGAACAGAGAGGTTTTCATTGACTCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
a	74 C T ...		---	AACAAAAACAGACACCTCGGCTCTTCTCACCAGTCCACATGGGTGCCAAACAATCCACATTCTCT ACATCTCCCACTGGGCTGGCTCTTCAACACCTACCAAGTCTTACCGGGAAGCATATA GCCAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
3	107 A G CCTCAGCA	CTCCTTCACAA GCTCAGCA	CTTCCCGGTAA GCCAAGT	ACTCACTGCTGCTTTGTTGATTATCAACCTAGCCG/AGTGTGATGTGGGATTAGAATAAAATA AACACAAAAATGAAACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGTAAGAT AATAACTTCAA
3	36 G A C		C	TGCATTCAATTATGCACCAATAATAACTTCTGTACAT/ATCATTATTGTATTTTCAACAAAAAT TATGAGTGAGGGATGATTGTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTACAGAGCGGGATTCCGAATCCATCAACTTGAATCCAGAGAAAAAT GTTCTGCATCACTGTACACACTGACTCTCTTTTCTCTCTTTGAAACAAGGC
1	37 A T ...		---	CTTCTGACCTGTTTGCAGTGGATCTGTTTGAAGGCTCTGCTCAGTATCTGAAGTTTTTGTCTCC A/GC/JAGAAGTCAATTTGTAGGTGTTCTGGGGTTTTTGTACGTTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGGCTTGCAGAGCATTTATCAGATGGCTGTTTGTCTGCACTTCTGCACTGAAG
11	70 G C CCA	CAGTATCTGA AGTTTTGTCT CCA	AGGAACACCTA CAAAATGACTT CT	TTTCATGAGAAGGTCCATGAGTTTACAGATCTCAAGGAAGAAAGGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTTGTCTCATGAAATTTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAAATCATCTATCCACGTGCAGAAACTGGCAATTTAGTTTTGT/TTTACTAAACACACAAATGT TTAATTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTTCTGTGATG
81	178 A T ...		---	CTATGATTCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTCAAAAGATGAGAACAGGTCCTA GAACCTCAG/GATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTACCCAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCACTTCTTATTTTGGCCACCTGTTTGT TAGGAA
791b	76 G A ...		---	

31a	44 C G ---			CTATGTATCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTC[G]ACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGCCCTATCTCACTGACCCAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTTCGCCACCCCTGTTTGT TAGGAA
36c	120 C T ---			CACTCTGCTGTGTCCATGGGTGCCACAGACTCTCCAGAAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAACCC[CT]TATGAGCCAC ACTTCTCATTTCCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGGAAAGGAAAGAGAGGCAA GG
06b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACTCTGCTGTGTCCATGGGTGCCACAGACTCTCCAGAAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAA[C]A[CCCTATGAGCCAC ACTTCTCATTTCCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGGAAAGGAAAGAGAGGCAA GG
06a	42 A G ---			CACTCTGCTGTGTCCATGGGTGCCACAGACTCTCCAGAAAG[G]GCCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGGAAAGGAAAGAGAGGCAA GG
38	48 G C TG	TTTATCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTT TCAAT	CCATTCCTCTCCCTCCCTTTATCTCCCTGTTTTCTTTG[G]CJATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
15	54 T A TTT	TCCTCATGAAT TCATCTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAGCAGGATTTGCTTCATGAATTCATCTTTCAGTTT[A]TAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
37	41 C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGAGACCTCCAGAGAAAAATCCAAGAG[C]TCTTAAACCATATTTTGTGTTTA GAACTCCTGTGCCAACCCACTCTTGATGTGAGTGAC
81b	131 A G CTGCAGTCG	TGTCATTATG	TTACTTCCAGG CTCCAAGTATT	AAGCCAAATTCACATTAGTTGATGAATTT[G]A/AAATTTACAGTATCTAATGCATGGGCATCTGTTTC TCTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCG[A/G]A ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
31a	29 G A AATT	CCAAATTCAC ATTAGTTGATG	CCCATGCAITTA GATACTGTAAT ATT	AAGCCAAATTCACATTAGTTGATGAATTT[G]A/AAATTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
92	38 T C ---			TCATGAGTCTTTCTCAAGATGCTTGTTAAAGTCCCA[T]C]CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

134	T C ---	CCCATACTTT TTCAGGTGAA	---	TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTTCATGCTTCACATTTATTTTTT TTTCACTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCAGTTTATACATATTTCTTTAGTTC TTTCAATTAATGCCACCATAGAAATAATTTCTAACCAACCAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCAATTACTCTTTACAC
40	CT A	CCTGTATTTTA GCAACATGGG	---	CCTTATAACCCCAATACTTTTTTCAGGTGAAAAAGGGGAAA[C/T]ACCCCATGTTTGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATTTCTGATGTGGGAAATAT TAGAAATTAAAGCGAGAGAGGCA
97	CT TTTTAGAGT	TGCACAAATTG CCAGG	---	TGTTGTCTGCACCTCCCAACAAGTGTCAATGAGCTCAAGGTTTTGATTGAGCGGGTATGGGT GGGCTATCGGCACACGCTTTTTAGAGT[C/T]CCTGGGCAATTTGTGCACTAGTGTGAGA TAAGTTGATTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAGAGAGAGAAATAAAGTGGATAGACATGAATAACTCTGATGATCTGTTGTATCOCTGAA TCCTGCAATATACACATGATTCAATGAT[C/T]CCATTTTGAAAAATTAAAGCTTTTGAATTGTTTTCCA ATG
b 161	CT ---	---	---	TCGGGTATTAGGATCGTTCAACCTCGATGATGGGCTTCAATAGGAGGTGGGA[C/T]TGACAC ATTACTCTCCAACGTTCATCAGAACACTTCAACAGCG
58	CT AGGTGGGA	GTTCAATAGG TC	---	CAGGAOCTTGGAGCCTTGTCTTTGTCTTCCACCTCACTCTTCTGCTGCCATGGTGGAGC CTCTCTCAGGCTTCTCTATGCA[C/T]GCGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCGA TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
b 134	GA ---	---	---	CAGGACCTTGGAGCCTTGTCTTTGTCTTCCACCTCACTCTTCTGCTGCCATGGTGGAGC CTCTCTCAGGCTTCTCTATGCA[C/T]GCGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
a 92	CT ---	---	---	TGCTGTATTGACACATAGTTATCTGACAGTAAATCATTTCAACATACACAAATATCTTATTTCTGCTG TCACACTAATTTGCAAGCATTCAATTGATTGACTATTATGAGCATCGTGTCAATT[C/T]CAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTTCTTCTGTAACCTCAAGTA
b 125	AT TTC	TTCTTTGAGA AACCTAAAC ACTG	---	TGCTGTATTGACACATAGTTATCTGACAGTAAATCATTTCAACATACACAAATATCTTATTTCTGCTG CTGTACACTAATTTGCAAGCATTCAATTGATTGACTATTATGAGCATCGTGTCAATTCAACAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTTCTTCTGTAACCTCAAGTA
a 44	TA ---	---	---	---
26	ACCGCAATAAA	GCCAAATTTAT CATCGAGGACT ITGGGA	---	TGAGAGCCAAATTTATCCGCAATAAA[AV/JT]CCCAAAGTCCGATGGAGGCATTTCAGAAATCGGG GCAGGGGAGGCAGAGGTTGAGACAGATGTGAAGAC



37	165	CT	---			GAGTTAATGAATCCTGTTCCCTCCTAAAAACCTCCTGTTCCCCCAAC TTCACATTCAGCAGATATT CTTTCATGGTTATTTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTCTCTGTGCGGTAT[C/T]TGCTCCAATCACCCATTCACATTTTATTTCTATTAT GCTGAATGAACGGTTATATTACAG
33	53	GC	---			GGGTAAGATCCAGAGCCACAGGTGAACCTGCGCGGTATTGAAGTCTTTGGGCCA[G/C]GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGACTGAGCCCATTTGAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACATTTTCAGCAAACTTGTGACGGTGAC ACACCATGCTTCGAGAGGAATGAGG
41	80	TC	AGGTACTT	CTTCTTAATTA AGCATCTACA	TGAAAACCCCA GAACAGTG	GACTCTGCTCAAGAAAAAATAAATTGAATAATTAAAGCACCTCTTAATAAGCAT CTACAAGGTACTTAT[C]CACTGTTCTGGGGTTTCAATCCTTTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAAATTTGCTTTT CTC
150	45	TG	TGTCACA	CCATGACTT ATTCTATATCT	TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTCCTCAATGACTTATTCTATATCTGTGCACAT/GIAGAAGTACCACACATTTCA AACAAGAGCCAGGCTATGCCAGGGTGGGATTATTTACGGTCATGTAATATGATGTAAAGACTA TTTTTACTGGCCTCTTTTATGTCATAAAACAAAGGATTGGTCTATTCAACAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGGTACTAGAAATAGTCTTTATAGAAATATGTGTTTAGAATAAGCCACA AATTATCTATAAACACACAC[C/T]AAGGAACGAGGCTCAAAAGTGGAAACAAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
161	88	CT	---			GAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCTATTCACTGAACTAGTTATCATATAAAGACATGCAAAAACCTTTTCACAGTCTTGT CCTGG[G/A]AATATCTCACAAAATTAATTAATAATGGCATGGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTT
166c	141	GA	TTTGCTCTGG	TTTTCACAGTC	AGTCGCATGCC AATTTATAAT	GAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT[C/T]ATTCACTGAACTAGTTATCATATAAAGACATGCAAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTAATAATGGCATGGACTTTCTGATTTAGCCTGACAGGA TTGTTCCCTT
466b	80	T	CTC	GACTTCTGGG CTATGAAATA	TGCTCTTTTATG ATACTAGTTC ACTGAA	TGCTTTTAAAAATAAATGACCACCACTGACACCATAGTCTGTCTCCATTTGCCACGCTTCTCTC AGTAGAATAAGACAGGACTTTGCTGGCTGCTATCT[C/A]TTCTCTCTCAGAAAGACACTTGGCCCT CATAGGCATTCCATAGATATTGTTGAATGAATGTGCTTTTTCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTGGCCTAT
814	104	CA	---			CCTCTAACAAGAAAACTTGACTCTCTCACTCAAAAATACCCTTCTCTAATAATTTA/GIAGTAACCA AAATATTCTTCAATAAAATTAATCTTTTAATTAGAAAGAACACAGTTAGAGGTAGTACATTCA CCACC
1720b	55	A/G	---			

20a	47	A G	---	CCTCTAACAGAAACCTTGACTTCCTCAACTCAAAATACCCCTTCTCTA/GIATAATTTAAGTAACCA AAATATTCCTTCAAAATAAATTAATCTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
25	123	A T	---	CACGCTTAAGGCAGGATGGCTTATGAGATACCTTGCAATGCTGCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTGCATGTGCAGATGAAGGCTCAGGTGCTTATGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTACCAAGGGTTAGTTGCAAT TAAGAATTGCCAGTCTTTTGCTGCTGCATCATCTTGAACATTATCCACATG
18	74	C G	---	CCACTTCAGTAAATCAATTTGTAGCACCTTATTTCTAAAGATTCTAATTTTATATGTTTACCCCTT GTCATT[C/G]TCAGACCAAGTAGATGTTTTCACACAGCCATCTTTCTTCTGGAAATCTTTCAGAAT TACAGTTATGATGTCCTTTTATATCCCA
43	91	T C	---	TGAGGTATGATTGCAGATTTGTAGTGAATACTATTAAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTATATCCATCTTC[C/J]ATTTTAAATTTTCTACTGAGCAGAAAAAAATGTATACATT AACCTTGTCTCCTATTGTACCTTTTAAATATGCAATTCACACCTTCTCTTTTGTATTAGGGA
31	39	T C	---	AGGGCCCTTACAGATCCGTCAGTCAACACTGCTCTT[C/J]AGTGAGCCTGTAACCAACCAAGAC GGCTGTGCATCAGTGTGCATCTCTCTTTCCGGACAATCTTTAAAGAAAAAAAGAGTGT CTTTGAATGTATCCATTTTATCCCCAAATAATCTTTTAAATAATCTTTATTAGCCAAATCCAAT GTGCTGAATATCTGCCAAGCATGTCTATCTACACAAAAGGGATTGCAAA
17b	84	C T	---	CTCAGAAATTTAGATCTTCCCCAAATGTGCATGATCTTGTCTCAACATCTTATTTTCTCAAAAC ATTTATCTAGCCTGT[C/J]AAGTGCATCCAGTGAGGCTGTTTATCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
17a	83	A T	---	CTCAGAAATTTAGATCTTCCCCAAATGTGCATGATCTTGTCTCAACATCTTATTTTCTCAAAAC ATTTATCTAGCCTGT[C/J]AAGTGCATCCAGTGAGGCTGTTTATCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
15b	115	C A	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCACACCTCACAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGGTCTTGAGCTGGCAGGGGGAGTTCAGACA[C/J]AGCCAAAGAAAAGCC TGATATTAGAGGGCACTTGCATTAA
15a	42	C T	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGC[C/J]ACCTCACCAAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGGTCTTGAGCTGGCAGGGGGAGTTCAGACACAGCAAGAAAAGCC TGATATTAGAGGGCACTTGCATTAA
13	146	C T	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGTGCCTCCCAATTTCTTTGTCTTGA TTCCCCAAACCAAGGTTCTCACCCCAATCTGATCAATGCTGACTAGGTCTAGGCTGGTCAAGGTAA AGCATTATGA[C/J]TAGACACAAAGACAAAGAGGTAAAGTTGCTGCTCCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

		TGATGTAATGC	TTGATTACTGT	ATATCAGTGGGTGAGTATACAGCAATCTATTGTTTATTATTTATGTGCTGCTATAAATCAATGGTTCTA
		TATGTAGCAA	GCCTAGGGGA	ACATTCAAATAGATCTTTTCTCTCTGCTCAGATGCTTTCATGATGATGCTATGCTATGAGCAAT
19	139	A T ATCT		CTA/T/TTCCCTAAGCACAGTAATCAAGGCTTCTACCCCA
		GCAGAAAAG	GACTGTTAATT	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTAGGC
		AAATCATGAC	TATTTAATCAT	ATGCATAGAGAAATAGCAGTGTGTTTATTGGCGAGAAAAGAAATCATGACTTTT/A/AAAAAATACC
2	122	T A TTT	TAGTCTGG	AGACTAATGATTAAATAAATTACAGTCTAGGGTTCCGGAGTGGCCTAAAGCACGCTAGTAGCCCT
				CCTTAGA
				TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTA
		TGTCATCTTGA	AAATTCTTTTC	GGCATGCATAGAGAAATAGCAGTGTGTTTATTGGCGAGAAAAGAAATCATGACTTTTAAAAATACC
		CTCGTATTAA	AGAGCCAGTTA	AGACTAATGATTAAATAAATTACAGTCTAGGGTTCCGGAGTGGCCTAAAGCACGCTAGTAGCCCT
3	39	T CATAAATT	AC	CCTTAGA
				TCTGAGTCTTCTGAGACACTTGCATGGTCAAGGGTAGCAGGATCAGGAGGCAATTATAATAAT
		CCTTAGATAT		ATAATTTGCAGAGCATCTCTCCTATGCACCAGATAATTGGTGACACTCTGTTTAAATCCAGTATCC
		ATTGTGATTGT	ACCTTTCTGAA	CTACTCCTTTAGATATATTGTGATGTTTACATG/C/T/GAAATCTGGCTTCAGAAAGGTTAGGTGTT
b	170	T TTTACATG	GCCAGATTTC	T
				TCTGAGTCTTCTGAGACACTTGCATGGTCAAGGGTAGCAGGATCAGGGAAGG/C/A/ATTATAATA
		GTAGCAGGAT	GAGATGCTCTG	AATATAATTTGCAGAGCATCTCTCCTATGCACCAGATAATTGGTGACACTCTGTTTAAATCCAGTA
		CAGGGAAGG	CAAATTATATT	TCCCTACTCCTTTAGATATATTGTGATGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT
a	54	C A CAGGGAAGG	TATTAT	T
		TCTCTGTGTTGT	ATTCTGTGTTGT	CCAGGGATTCTCTCTGTCCTCCCAAACCTCTTAT/C/T/TAATTCATTCAATACAACAAGAAATTTATAGAA
289	29	T C CAAACTCTT	TTAA	TATGCACACATGCCACAAGACACCCCTTATATTAGT
		TGGCACTTAG	GCCACACACCC	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATCTTTTATJACCATAGGGGTGTGGCTTATCT
		AACATAGTTT	CTATGGT	TTTACCTGGCATGGCTTAGGTCCTGTTTATAATTTGGTATCTTTTGCCACAAGAGTCTGTCTGAC
119	40	A T ATTCTT		AGTCTTATGATCTCTATTTTAACATTAACACTGGTCAGATGTGTTTAAAACTTGTGAACCTGCAGC
		CTGTTGAATTT	GCTTTGGAATG	AGCAACGTGTACAACCTTAGTGAGGTGTAATCAGAAAGCATCTATATTATTCACAGTCACCCCTG
		CTACCTCTATT	TATCCAAAAGT	GACTATAGTCTGTGATTTTCTACCTCTATTCTCTTAT/C/T/AACTTTTGGATACATTCCAAAAGCAT
316	104	T C CTCTT	TT	CATGGTCACTTCCAGTTATGAAGGATGTTTAAAGCCCCAGCC
				AGTGAGTTGTGCACAATTTGGAGACATCTGTGACCCCCAACTTAAACACTTCTCCCACAC/C/T/AC
572	61	CT ---	---	AAAGTTAACACTTCAGTTACAGGTGATGATTGAGCAGA

38	31	C	T	TGAAGCAACC	CAAGATATTAT	GAGGAAGCTGCCTGAAGCAACCAGGCTGTGTTGCTCTACCCCTCTTAGAGAAATAAATAATATCTTT
				AGGTCTTGTT	ATTTATCTCT	GAGATAGGGAGGAGCAGCCTGAGGACAGCTGGGTTTTGTTCTACCCACTGGAAGCAGAAATATCC
					AAGAGGGG	TTCAAAGCTTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGCCCTTTCAGGG
31	32	A	G	CTGCTCAGGT	GGGAGTTAGGA	T
				GTCAAGAAGTT	GTCAAGAAGTT	CCTCCCGTTCTCTGCTCAGGTATGACTCCCAGTCAACTCTTGACTCCTAACTCCCATCTCGGTG
				GA	GA	TCTGCTTCCCAGGGGAGCATCTGACACAGCCTTTTGCCTTGTCACAAACAGAACATTCGAGAAG
						TGATGCTGCGTGACCTCCAGGATA
				GTTACCCAGA		AGCGATGAAATTTATATGTTATGCTTGCTGACTTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT
				GTCCTCTAATA	TGCGGCTTCCA	TTCCAAATTATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTTT
146	A	C	G	GTAGCT	GTAGCT	CTAATAGCAAACJAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
						AGCGATGAAATTTATATGTTATGCTTGCTGACTTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT
				---	---	TTCCAAATTATTAATACJCTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAG
						TCCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
				GGGTGCTCAAT	AAAATCTGTT	AGCGATGAAATTTATATGTTATGCTTGCTGACTTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT
				AAATATTATT	GGTGAAATTC	ATTTTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGT
				CTTTT	TAG	CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
						CGTTGGGAATTTCTATCTCACCTAAATATGCGTGATTAATAATATACATTTTAAACAACTTCAAA
				CAAACCTCAA	AAATCCAA	TTGCTTTAAGTACTTTACJGGAAGACCTTGACTGTGGATTTTGAGTTTTTCTTTTATCTTAATA
				ATTGCTTTAAG	GTCAAGGCTTT	AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT
				C	C	TATGTATT
						CGTTGGGAATATTCTATCTCACCTAAATATGCTCAJGATTAATAATATACATTTTAAACAACTTC
				GGGAATATTTC	GCAATTTGAAG	AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGAGTTTTTCTTTTATCTTAATA
				TATCTCACCTA	TTTGTTAAAT	AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT
				AATTATG	GTAT	TATGTATT
				CACAAATGTA		GTTGGAACCTCCAGTATCATTTCCCTCAAACCGCTTAAATCAAAATCACTTTTCTTCTGTGA
				ACAAGAATTG	CCATGGCTGTA	GAGCTCAAACCTCAGTCTGAATGAATTTGCTGCACAAATGTAAACAAAGATTTGATCCTATTCJACTGGG
				ATCC	GTCCAGT	ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAAACAG
				CAAGTGAATT	TGCTCTTTCA	
				ATGACCAAAA	TTTGAGGTTTT	TGACTCAAAGGAAACACACAAAAAGTTTACCACAGTGAATATGACCAAAATGAGAATCJAAAT
				TGAGA	T	TTGTTAAAAAAAACCTCAATGAAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTGT
						ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTCTTTCTTTTCTTTTGTGTCCTTA
						GAATCCATTTTGTCTTTTGGCCAGCATCCCTCTCCCCATATTTTAAAGGAGAGAATTCACCTTTTCT
						CTGTTGGATGATCAGAGTTCTGCTCTCCCAATCCAGAGGAGGACTACTATTCACCCCATGGGGTCAT
						AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTGAAAACC
56	59	T	G	---	---	



154	T G T T T T	TTAACCAAGA GTTTTTCATTG	CTAACTTAAAA ATCCTCAATCA AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTAAGCCTAAAGTAGTGTCTTTTAACCAAGAGTTTTTCATTTCTTTT TTTAAAAAAGAGCAGACATG/GTTTTATCAIGTGTTCTGATAAATTTTTTATATATTTTGAATGAGGATT TTTAAGTTAGCAT
95	A G T T G A A A A	AATAAGTGAA AGTAACTGAC	AACTCTTGGT TAAAAAGCAC TACIT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTAAGCCTA/GAAGTAGTGTCTTTTAACCAAGAGTTTTTCATTTCT TTTTTTAAAAAAGAGCAGACATTTTATCATGTGTCTGATAAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
5	25 A G ---		---	CAAGTGCTTGACCTTGATAGGTC/GA/C/CGGCTGAAGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAAATATAGATCTTGTCCCTTTGGGTTTACCAC TAGGGTGCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATTCAAAATAGCCATGGGTTGGACAAAATAC AAGGTTAGTGCTCTCTAACTTTAATGGGCATA
16	133 C T A A G G	TGCCCTGTGC	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAAACTAGAGCCCATACAGAGTGTATGTTAATATATGAAA AAAGTCAAGAGAAAGATGATAGTCTGCTAGAATACTTGAAATCTGATGCCCTGTCCAAAGG C/TTGTGCTACACATGAATTTAGAGATTGAATGAAAATGGCAAAATTCAGAAAAGGG
75	77 T A A	AAATGATTCTT TCTGCTCAAAG	CTGTTCTCACA TTCTTTTGA AA	GGTAGGATGATTCTAGATGCCACTTACAGCCACTGAAATATATGCTCCCAATGATTCTTTCTG CTCAAAGAGT/AJTTTTTTAAAGTTATCTACTTATTTATATCTGCTTTTTCAAAAAGAAATGTGAGA ACAGTACAAATGTTTCAGTATAGCAAAATTAATTAATAAGTAAGAAAAAGAGCCAAAT TGGGC
144	A G T A T G A G T T T C	TGCAAAATGCTT TATGAGTTTC	GGCATTTTGTA AAGGAGGAA	TAGAGAGGCTTTTTCAGTTTCAGGGTTGGAGGGGTTGGTGAGATTCACTTCTTAGAAGCACTGGC TATGTACAGAAAGATAAATCTCTGAGAAAGAACTCAGTTCTAAAGTGTTCAGTCTTGCAAATGCTTTA TGAGTTTTC/GJTTTCTCTCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCT T
23	T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTCTC TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGCT/C/GAATGACAAACAGAGAGAAAAAGAGATAAAGGTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCTCAGTGCATGGAGCAGTG
19	115 T C G C C A T T C T A G	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCAACTCTGTCAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTTCTCTGTATGT GCCCAACATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTTCTAGT/C/GGCTGCTGGCAGTGT TTCAGCCTGCTGCCCACTAACTAA
21	40 A G C T T G C C A	TGGCTCTGCTA	GAAACTCCAC ATAAATAAAT CTCA	CAACCAATTGAGATTTAATTTTGGCTCTGCTACTTGCCCA/GATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTCCCTGCTAGGTTTTGAAGAAAGTTGAA

88	T C ---	---		GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAACTTTCACCTTTTTCATTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAAAGCTGAGGAAATTTATTCAGAAAG GCAACATC
80	T A AACTT	GTAAAAGGG TGATAACATAA TACCTTT	GTATCAGTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAACTTTTCATTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAAAGCTGAGGAAATTTATTCAGAAAG GCAACATC
2	80 C A ATTGGTTCACT	GCTGTGCTTC CTTTAA	AAGAACAATG CATAACAGAA CTTTAA	ACATGTAATTCCTTTAGGGTCAGCCTTCCTACCCCAAGAATATCCCTGGTTTATTGCTGTCTTC ATTGGTCACTTCATTAAGTTCTGTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACTCTGTTAAACTGTC
6	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGCTTTTCTTTGTACGAGTGCATAAAGAATTACCACTCTGTACATTTTGTAAAGATAGCACAG AGAGAAGCAATTACAGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACTC(AT)CCAA CCATTAGGATTGTCACCTCATATATAGACAGAATTCAGTGGTGGTATTTGAATCCACACATGGA ATAAGTCTA
5	68 C T ---	---	---	GAAAWAAAGTTTAAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTTCAGATTATTTTAGT [C/T]ATTTTCTTCTATATATTTCTTGAAGTATGATTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTTATCCAAAGCCCCATTCCACCATGT TTT
89	G A AGAGAAA	GAGAGAATAT TCCAAAAAGT TTCT	GGTCTCTAAT TTTCTACACT TTCT	ATGAAAAATGCATTAGAAGATTGGAGGATAAAATTTGAGAGAATATTTCCAAAAAGTAGAGAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]AGAAAAGTTAGAAAAATTTAGAGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
18	G A ---	---	---	ATGAAAAATGCATTAGAAG[G/A]AATTGGAGGATAAAATTTGAGAGAATATTTCCAAAAAGTAGAGAA AAAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGGTAGAAAAATTTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
136	G A GGCTGG	CATACCACTGC AGTTGTGA	AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAAATGCTAAAAATTTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCCTGCGGCTG G[G/A]TCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAAATGCTTTACACAGGCTACTGG AAAGCC

25	C	T	A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTCG	AGCCACAGTGGAAATCATTACACTA/C/TGGAATCAGCAATGCTAAATGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCACCGTTGAACATTGTTAAACATTACCAGCATACCACCTGCGG CTGGGTCAACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAAATGGCTTTCACAGGCTACTGGA AAGCC
75	39	C	T	CACTC	TTTATGCCATA TTAATTCAITTA ATATGATG	TTGCAAGTTGTTTTATGCCATAITTAATTCATTACACTC/TJACATCATATTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGATATCTCGCACGATAATCATTGTTATCATTAGACATTGCA GGAACCAACATATGGATGGAATGTTGTTTAAATGAAGGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTTAAGTAAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/C/CJGACATAGTTGCTAAGGATAITCCACAAAATTAT TTCATGA
26	165	A	C	---	---	CAGTGGCTGGCTACTGACAAAACGTAACTGTCGGCAGGTGGCAAGGGAGGAACATTACAG/A/GJG TCCATCTCTGATGTCAACAGCAGGGGCCAGGAAGGTTGATCTGGAG TGGACACACTGCTCTAGACC/C/TJCCAGGGTCCCTCAAAAGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGACCCAGAGGCATCAGGGCCCTAGTCTCTGGGACAGTGAAGGGCCCAOCC
78	62	A	G	G	CTGGTGACATC AGAGATGGAC	ACAGAAAAATGCCTAGGCTTTGTAGCAAGAGAGGAAGCATCTTCATGGGCAGGAATT/C/JCATTT CTGTGTTTCTTAGGGTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCTGATCCAGCAACATT TCCGTAACCTACCCTCTAGAAGTCATGCAAGAGAAATGATGA
89	21	C	T	GCTCTAGACC	TTGAGGGAOCC TGGGA	GGACCAACAGAAATTACTTGGCA/C/JAGGGTTCTTAAACATATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATATTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
128	23	T	C	---	---	TATGCCCTCCCAAGGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGATACATCTCTGAATG GGCAGATTAATCTGCAGGCTCTCC/CJ/TTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGGAGGAGATGAGAGAAAGGCTGCTCCGTGAATAC TAGTTCGG
132	91	G	C	AGGCTCTCC	A	GATTTGAGTATTATCAAAATTTGCCCAAGACCATTAAAGATTTAATAGTTAAAGCCAAAACATA AAGAATTAACTGTTCAAAAGTGTGTTAAT/C/JCTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCACTAAATTTCTAAAGTCCAGT
134	96	C	T	GTGTTAAT	AG	GGATGATGTTCTGTGGTCCCTTAT/CJAAAGCCTCTTGATCCCAAAATGTGTAAATTTATTATTCT TGGTATTTCTCGCTTACCATAGTACCTGTCAAGTGTCCACCCCT
37	24	T	C	---	---	





3	33	C T G T C	CCAGTTGTA GCATTCAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCTCCAAAGTTGTAGCATTGAGAGTGCCTCTCTTTAGAGGTAGTTGCTCGTCTGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTACCTCTCTCCAAACAAAGTGTACCAACAGCAATTGTTAAG GAAATGTGCAATGCTTGTCTACCTCTGACGACACATAATTAATCCCATTTGCCTAAAAAGACCAGG
3	70	C T A T C	TTCITAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCTACAAACACAGAAATTAACAAATGAAATTCAGCTACTCTTCTTAGGCCATCAGAG AACTCTGAAGTATGAGGAAATTTGATGCCATGTGAATGGAGAAACAGACAGGCATATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCTCTGTAAGAC
4b	109	G A ---	---	---	CATGCTAGGTAGTCTGATCATGAAGTTGAACAACTTAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTAATGAGGTGGTGGGAGAAAAATTTGATGTTGCG TAGTTGAGTTTCTGTCCACC
1a	90	A G A C	AGTCAGTTTCC CTAATTTTAGC	CAACCATCAAT TTTCTCCCA	TTTGACCCCATACATGAGAAATAAACCATAGAATGGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTCTCTTGGAGCAGGGTCAACCCAC
2	79	C T G G A T G T C T	CCTGGGTTTCT GGATGATGCT	GGGTGAOCTG TTCTCA	TCACGGCAAGTTCTGCAGCAGTGTCTTGAACCTCTGCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTGTTTCTGCTTAAAGTATCCAGAGGTGTTTCTAACCTGGATA TAACATCTGCTATGGAAGGCTGCACCTGGATGAGGTCAAAA
0b	146	G C C A T C T	GGTTCTAACC TGGATATAAA	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGAACCTCTGCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTGTTTCTGCTTAAAGTATCCAGAGGTGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTCAAAA
0a	78	T G A T A G T T C T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TAAATCATGCTTATTTTCAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAGCTCTCATGCTCTTCTGAACTTCTACTTACTGTGCTGTTATGATGCACCTGTCTCTTTGG ATAGATGGTTGATAGGAGATGGGTGTTAAAGACACAAATTAACCTTGTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTATCACTGAATGAGTCCAAAAGCCTTTATGCTTAC
8	125	G T ---	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA TTCJAAAAAACTACTATAGTTTATGAAAAATGACTTCCAAAATTCAGAAAAAGTCACTTAAACAGG ATTCTCAATTCAITCCAGAACTACTCTCTGTCAATCTTAACCTTGAAGTGCACAG
7	67	A C ---	---	---	TCTAAATGTGAAACCAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAACCTTCJACACCGGTTCAATGAAAAAACAATGATTGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTTGGGCAATTAACCTC
5	72	T C A A A C	CCTCAGTTATG TATCAAAATGA	GGCTCACAAT CAITGTTTT	

19	51	CT	...			GAAAAGCAGGAAGCCAGGACAGAAAACCTTTGAAAAGCTTTTTCAGCAC/C/TTCGTGGATCCG AATTTTAGTGTGATTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTCACATTCACACAGAAATGTC CAGATTAGCGATTGTTGACTTGCCAAATTAATGAATGTGAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC
46	116	GA	...			GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGAATGTTGTTCTTCATCATCTCTGCTGCG/A/GCCCCAGGATAAAGCA GGCA
37	49	TC	CAA	ACAGTCATTT AGTCTTCCTGA	TAAGATAACC ATACTAGGTAC ATCOG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTCCTGACAA/T/CJCGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTACTTGAACAAAGACACAGT CATTAAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
38	25	AC	G	TGACCAATGTC TTTAGAAGCA	TOGTCGGTGC CTCTOC	CAATGACCAATGCTTTTAGAAGCAG/A/CJGGAGAGGACACCCGACGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCCAACAGGTGAGGAAGAGCAAGGGTTGCTGGCCACT
01	114	AG	...			GGACATTGTCCTCAGAAAGTACATTCAAGCCCTGGACGGTGTCTGCTAACACTGTGACCTCAGGCA AGTCATGCTGCTTCTGAACTCGGCTTCTCACCTGACAAAGTG/A/GJ/TATCATGTGCTACACTGC AGTGTATATGCTGCAT
14	99	CT	GC	TGATTCTTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACCTGAGGAACCTTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATTCTTCTCAAGACTCACAGC/TJACCATCCTTATTGCTTAGACCTATACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAGGTACAAAGTGTGACCCATGGGAGGTATGTTAGGCTA CAAAAGAG
19	33	GA	A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	CCACTCCAGGCCAAGAGCGTCTATGAATCAT/G/A/CATTGTTCCTGTTATTGCTGTTCACAGAT GGCAACTCTTGAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAGGGTIC
91	84	AT	GTCAATGCATG	TTGAGGTCCTTA TTCATTGCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT	TAATTACATTGCTCTGTTTGTGCAATTTATTGCTTCTTATGTAAACAAATCACCACATTGAGG TCTTAGTCATTGCATG/A/TJGTATAACAATAATTGTCACCTTAATAGGAACCTCAAGCATAGTTATGIGT ACATTTATTGCTAACAGCAG
60	117	AG	CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTTCTGTATAGGAAGTCTGATTAGATGCCCTTTGAGGTTAGTTGGCTTCTAAGATGGTAAT ATCTGTCCAAGTTTTTTTCTTCTAATAATTTAGCAACAATATCAACAGAA/A/GGGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
68	32	AG	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAATTTGATACAAACA/A/GJ/TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATACCAGCAGTGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

7	68	T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTCGGATATACCTTCCAAATGACTAGTATGAATAAGCAGCGTATTAAATTTACCTATTATATTT AT/CJ/CATCATGATTTGCTGGCTCTTCCAAATTTACTACAAATTTGATTGTACATGAGGCACATG ATCCCATTAACCCAAATAG
9	51	A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTTG	GCCATGAGCACAGAGGCTGAACCACCTCCCCAAGTTAGTCAATATAAAAAA/CJ/CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAACAA
3	24	C T	CTGTCACTGGT CTGGCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACGTGCTGCCCTG/C/TTGGCTGTTCTCTGTTCTTCAATGTTCAACTGCTTGTAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAATTGCAACATTTGGGCAT
3b	117	A G	...	...	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACAGGGGTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
2a	94	G T	TCAATATGAG TCTGTGAAC AGG	CTTTTACAGGA TCCTTCCCAC	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACAGGGGTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
5	68	G C	TGCTCCCCCAT CACCT	G	TAAATGCTCTGGGAGATAATAGGAAGTCCCATCCCTCTGATACCTTGGTTGCTCCCCCATCACCT [G/C]CTTACACAACCTTGAAGTAGGCCCATCCAAACACTGTGTCAGAGAGTAACTGTGAC ACAGCCTCTTCAAATGGCACAAATCAAAAGCACACAGTAAAGAGCAGAGGCAAAATCTGG[C/T]CTCAC CAATGGAAAAGTCTTCTGAAGGATAAGGGAGTGAATGACTGCTAGAGAGAAATGATTGGCCTT
8	57	C T	...	...	AGTTCACCTGCCTAGATGAGTAGACCATGTTGCTTTGTTAAATGTACATGGGCAGGACCGGAAATGG GATG[C/T]TACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
5b	71	G T	...	...	AGTTCACCTGCCTAGATGAGTAGACCATGTTGCTTTGTTAAATGTACATGGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
3a	58	C T	...	...	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGGTTAACTGGATGCCACTTCTGCTGTCAOCTTCT CTAGACTCTTGACCTGCAGGAGATCCCTGGCTCCTGAGTTTATCATCTCCACCTCCAGCCCCAG GGCCTGTATCTGTTACAGGCC[C/J]GAAATCTGTCACGGCTCAACTGTGGAGGTAGGAATGACGA G
7	158	A G	...	...	CCAGTCTAGGCTGCAAGGACTTCAATCTGGGGCAAGTCTGGTGTGCTAGGTCAGAGGCGG ACCTGAGGGACACAAACCAGTGGGACACCAGGGGTACTTGTATCACCT/CJ/CTCCCGCAACCCCA AGCAGCACAGCTTGACGCTCAGGAAAGACTCCTTACTCCACTTGAGAAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACTTGGGA
6	117	T C	...	...	



1	54	C	T	...			TAGATTTGATTGATGACAATAGGGAAGCCCTTTGTTAAATTTGGGTTTGAAGAA[CT]TGAAGAAAA TGAAAGGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAAAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
3	70	A	G	CTCAAAA			TTTTCCCTTATTTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[AG]GCGGAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
3	112	T	G	ATATAA			CCCTGAATGTGCTTTGCTTCTCTCAACTCTAGGGAACTTTTCCATGTGAGGTTTGA AGAGTACTTTAATTAACCTTGATCAAGAGATGGGTATATAAT[GT]GAAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
6	49	C	T	TATAGTTCC			ACACATTTCAATTTGCTTTAAGTTGAATTATTCAGAAAAATTATAGTTCC[CT]CAAGTTTCATGCATAA CAGGAACACCCAGGTTGGGCAATTGATTGAATTGT
1	49	A	G	CCTCC			CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAATTTATCCTTCC[AG]TGAATTTGGTGA GGTCAAGAATGAATTCACCTTTTAGATTCTGAAATTTTATTTGCGATGATAATGCAATGGGC
5b	75	G	A	...			CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGTATATAAAGAAAAACAGTTAGTAATCTT TCACCTTT[GA]TATTTCTTCTACCTCAGGGAATC
5a	41	A	G	ACACGAAAGT			CTACTGGATTTTACTTTGCTCAAGCCAGACAAACGAAAGT[AG]TATAAAGAAAAACAGTTAGTAAT CTTTCACCTTTGTTATTTCTTCTACCTCAGGGAATC
9b	160	T	C	TAATC			GGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCAATATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGTGGCTGAATATATTTGAAGAAATAAA GGAGTGAATAAATGAATGCCATAATCT[CT]GTGTGTTTTTTGTCCCCACCTCTCACACCTTTCCCTGG CACA
9a	86	T	G	ATGCTCTGAGT			GGGGTTAGGAACCTCGAGATCTTTCAGAAAGCACAATTCAAACCAATATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[GT]CAAGGCTGCTGACATGGTGAATATATTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCCACCTCTCACACCTTTCCCTGG CACA
9	64	T	C	AAGATG			TGAGAGAGTTTTTGGATTATTCATCCTCTGCAACACTCCAAAGTAAGTCTATCATTTCTGAAGATGT[CT] GAGTTCTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTATTTTGAATATATAAATCTCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGTCCGTGGGACAAAGATGGGCCCTTAGGATCATTTT

10	110 A G	GCACATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCTTTTCTTAAAAATGGTGGCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCCTAT TGCTCGGTACAGTACTTTGCAATAAGCACCATGTGGCATCCAGTGGATGGCTGCTTGTCCAGTC AAATGAGACAACTTCTCTAT
12	226 T C	---	---	AGCAAGCATCTGGCAAGCCCTGGTGACCAAGACATTAAATTCACCAAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATCTCTGTACACA AATACTTTATGGGAGACAGCATTGTAATTCAAATCAATAATGACTCGGTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT/CJCCCTCTGCTAGAAACCAATTGAT
15	105 G C	GCCATTGAGG AAGTGTTTAA	GAATGGATGGG TCATCTCTCT	CAAAGGTTAGTTTAACTTGGGGGGCAACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCAATTGAGGAAGTGTAAAG/CJAGAGAGATGACCCATCCATTCTCTGG GCTTCTTATATGACACCACTACTATCCACACAGATGTGGAGTCATTTATTTGGTGTATGACAGT CATGG
18b	99 C T	CACTGTTTCT ATTGACCGTAC	AGAAAAAGAG AAGAAGGGAA AAA	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAAACGCCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG/CJCTTTGCTTTTTTTTCCCTCTCTCTTTTCTG CCCTCTTTTAACTATT
18a	38 G C	AGTTGTGCTG CTACGTGTT	TTTTAATTTTC TGGGGTGTCT	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTAG/CJAGCAACCCAGAAAAATTAAACGGCC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTTTCCTCTCTCTTTTCTG CCCTCTTTTAACTATT
16	69 T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTTGCTCTGAAGCAGAAAGCACTGTGA CT/AJCATTTATTAGGCCATCTCTCGCTGGAAGCCCTGCCTACAGCAATTGTAAACATATGGCATTTGGG ACATATCTCTGAGCCCATCAACTATTGACAAGATTCTCCTTTTAAACAA
12	119 A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAGTCTTGGGAAAAGGATTGTGATGATCATTG AATCTGTTTAAATACAGAATTAATCTGAATACCTGTGTGAATCATTTGCTTTCJACCATGTACA TATTATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
16	61 A G	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAAGGAAAAATGATAACCAAGGACTGTTGTTCAAGCAATGCTAGAAAAATTATGCTA/AJ/C CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAGTTTCTCTTTGTCATTAAAGTCTCTATTCA ATTACCATTTATCGGGGTAAATAAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
7	77 C A	GAGGCATGAA GCAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGGGGCAAAATTAAGCATATGAAAAATACCAAGTGTGGCAGAGGCATG AAGCAAAAGAGG/CJCTTTCATCTGCCCCCTGGTGGGTTTTCAGTAACAGCAACATGCTTTGCTCC CGGATGAAAGATACCCCTCTATGACTCAGCAATTCACACTCCTAGGTATGCCCTTAAACATGGGTG GCAAAAT
19	50 C T	GAGACCATTTCT TTCCGAATG	TGTAAGGTG TACTTACAAGA AATCATC	TCACTGTTTAAAAATTTCTTCTCTCAGTGAGACCACTCTTTCCGAATG/CJTGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGTAATTTTTTAA AAAACTCTCCCAATATTG



					TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTCACTCACCATTGCTCTTATTGCTCTGCAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAACTGTCTTTAAAGTGTGAAGTATTTA ATTAGATTCTATTGATAC/C/TTGATGTTCTTCAAGAGGAAATTTGTAAGAGGATTCCCAIT
155	C T	ATTAATTAG CA	ATTCCTCTTG AAAGAAACAT CA		TGCATTCCATTGGC TCATTGACITTTTAGAGTCCCTCAGTCTTTATGCTTATTCTTAGGAAAACTAGGCTAGGAGAA CACAATTCAGGTTCTCTCCAGATGCAGAAGATACTAGAAAAATGC/C/TTGAACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTTTCCAGAACGATTAC
113	C T	AATGC	GGATAAAAT AAATTTTGGC ATAA		AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAACTCAGTGCATAGATCATCTTCTAAGTTCC/C/AG TTGAAAAAAATTAATGAAAAATTTTAAATTTTATCCAAACCTTTAAGTCGAGATTATAATTGATATTT AAAAAATATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
65	A G	TTCC	CTACTCTTCT ATTCATAATC CAAAAA		CTTACTCCAAAGTGTTCAGAGACCACCTTCATTC/C/TTTGGATTATGAATAGAAAGAGT AGGTTTATTTATCTCTTTTACCAAGGTGAATGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGAGCCA
38	T C	CACTTCATC	CCTTCCITTTA TATGATGCCA GA		TATAATGTTTTTGTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATCAAGAAGGAAAAATATACATATGGGTGATAATGGGCCCTGTTC/C/CTCTGGCATA CATATAAAGGAAGGCTAA
121	G T	GGCCTGTT	TTGCCATAGAC CATATGTATAT TAGGTTATGTC		TATAATGTTTTTGTCCATAGTTGCCATAGACTAGGTTATGTCC/C/AG/CACATGAATAAACAATCTTAT ATAATAATTTATCAAGAAGGAAAAATATACATATGGGTGATAATGGGCCCTGTTC/C/CTCTGGCATA CATATAAAGGAAGGCTAA
3a	43	A G C	AATAAAT		TTTTTCCATTTTGTGATTCCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGTTAAT AATATAATATATGATGTTATATATTAACAATTTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA/C/CGACTCAITTCCTTTGTCATCTATTCTAGGTTATTTGCAGCCCGAGATCTACCCAGG
7	139	T C	GATGCAAGA AGAAATGAGTC C		AAATGAGTAACCCAAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA/C/ATGAAT AAATGAGTAGTGGAAITGCTTGATAACTGGAGTAGTGCTT
3	56	G A	CAATTCCACTA CCTCATTTATT CA		AACATTTTTAACCATGCTACATTTACAAACACTGAAAAGACAG/C/AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAAAAT AGAAACACGTGATACCTGGAAGGAG
3	44	A G	---		GCCTTTTGTAGTTTAAAGTCTTTTGTAGTGTGCTTTTTTTTCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAGAAAAATAAGCGCTTGG/C/AG/GATAAACACATCTTC
7	93	A G	---		CCCTGCTATAGGTCAGTTTAAAAATCCTG/C/CCCTGCTATGGTTGCTTGTGAAGCCACATCCACT GAGGTATATTCTGCTGCATTTCTATATCACTCAGCTTTCAGATCCCACTCCCACTCAACTTGCAG
5	29	G A	---		



2	232	C A ---	---	GGATAATCAGTACAAATATGGGACCTTAAACTGCTGTGATGCAGGAGTGGGGCTGGCAGTG CCGAGGCAAGGGAGGACAGTGGGACAGGGATGCTCAGTGGTGAGCCACAGCCCTGGGCTTGGA TGGGCGATGGGAATGACAGGTTCCACATCATGCACAGAGGGCTGTAGCTTGATCCAGACAG GCTGCCACATTTGGTGTGCCCCCGGCTA/C/A/CTGGAGATGTCTCTAAA
4	138	C T ---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATTCCTTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTTACCTCTTGTCATTCACACATCTTTATAGAGAAAT/AAACCCAAATTT CT/C/TTTCAACCATTTAGTTTGAATATCATCTGGATTTTCACTCAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACTTTAATTAATTAAGGAACAAT
4	123	A G ---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATTCCTTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTTACCTCTTGTCATTCACACATCTTTATAGAGAAAT/AAACCCAA TTTCTCTTCAACCATTTAGTTTGAATATCATCTGGATTTTCACTCAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACTTTAATTAATTAAGGAACAAT
5	74	C G ---	---	TGAGTCTGAGCAGGAGTTCAGCCAGGGCCAGTGGGAGGGGTCTGGCCAGTGCACCTTCGGGGGCG GCATCC/C/G/TTAGTTTCCACTCCTCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTTCTGTTGGA GTTGTTCAATGTTCTTTTAA
3b	42	T C ---	---	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAT/C/CAACAGCAAAACAAACCCACA CAACCCAAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTATTTTTCATGTCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTTATTATTATTTGTTTCAAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTC
3	56	A C ---	---	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAAAACAA/C/CAACACA CAACCCAAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTATTTTTCATGTCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTTATTATTATTTGTTTCAAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTC
17	41	G A O O C C	---	GTGGCCATCGATCTGGACCGTCCCTGCCACTTGTCTCCCG/A/ATGAGCACTGGGTACAACATCCA AAAGTTCAACAAACCCAGAACTGTGTCTCATGGT
38	180	A G ---	---	TATACCACCTCCATTTGATGATGGAATGCTGCTGTTTCATGACCACTTTATGGCTAGATGGTTCAGAA AGCACCAGTTTCATGATAGGCAGTTTCAGGTCAATATGTTGACTTGTATGACCCAGAGTCAACATTCAG TTTCCACCAAGGCCAGTAACAGGCCAAGAGCTGTCTCTCAAAAG/A/G/AGAGTAGTTATCTGCAGA AGATGGCAGGGCTTGTCTCCGAAAGCCTAGAGAGCCGCCACTGTGATTCACCT
05	26	C T G G G A T C T	---	GGTCCACGAATTTGCTGGGAATCT/C/T/G/TTTTTCTTTAAGACTTTTGGACATGTTTGACTCC CGAACATACCGACCGCTCTCCTGTTTTTCTGGTGG

46	G A ...	...	TTTGTGTTGCTGTGGACACCCACTGCTCCAGGATGAAGGAGAG[G/A]AATGAGATCAGTTTGGGA CACTTCCTCTTGAATATAAAGATCAACAAGTTACAGTCATGTTGGGACTTCTCTCTCTCCAA
78	A G ...	...	AGTGCACTTTGGGGAAAGGGCTCCAGTGTATCTGGACCACTTCTCTTCTTTCAGTGGGACTCTT GATCCAGAGA[A/G]GACAAAGCTCCTCAGTGAGCTGGTGATATATCCAGACAGAACCCCAAGTCTCC TGACTCCTGGCCTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCACTTCTATCCAC CTATTCTCTGAAAATATTCCTGAGAGAGACAGAGATTAGATAAGA
43	C G GCCATC	GCTCCTCGCTG GGTCA	GCAGAGAAGAGAACCATGCCAGGGAGAGGCCACCCAGCCATC[G/G]TGACCCAGCGAGGAGCCAA CTATCCCAAATATACCTGGTGGAATATACCAAATCTGCATCTCCAGAGGAAATAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAA
53	A C TT	TCTACTTTCTG OCTTGGGT	AGCAGCCATCACATGATCTGTTTTCCACCATTCTCACTGAAGACACCATTTAT[AC]TACCCAAAGGG CAGAAAGTAGAATTACTATTCATTAATGTTTGACACAAATGGAATTGTC
293	T G ...	...	AAGGGCATTGAGACTATAAAGCAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAAGTGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTTCTTATTTTCTTTTCCATTGCT TATCTTGAGCACAATGATAATCAATTATACATTTATACATCACCCTTTTGACTTTTCCAAAGCCC TTTACAGCTCTGGCATTCTCTCGCTAGGCCGTGAGGTAACCTGGAT
38	A G AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCGGAGGTAAAGTTCTTTTGTCTATAAAGAA[AG]AAGGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAAATGTAACGT
249	C T ...	...	GGAGTTGCCCCCTCTAAGGGAAGGAGATCTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGTGGCAGGAGACCTTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAGGAGGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTTCATGCT GTGAGGCCCTTGACCCAGGTGGGGCCACAGCACAGCAGCATCTTTC[CT]
157	C A ...	...	GGAGTTGCCCCCTCTAAGGGAAGGAGATCTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGTGGCAGGACCCCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAGGAGGCC CCAGGCTGGAGCAGCATGAGGG[C/A]CAGCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTTCAT GCTGTGAGGCCCTTGACCCAGGTGGGGCCACAGCACAGCAGCATCTTTCGT
34	C T AAGAAC.TCA	TGTAGGGCTGA GCTGGC	CATACATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTCATGAAGGGCAAAAGGAGTGCCATGCAAGCTGTTTAA
61	C T CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTAGCATTACCCCCAACCTCATTTTAGTTGCCTAAGCATTCCTGGC[C/T]TTC CTGTCTAGTCTCTCCTGTAGCCAAAGAAATGAACATTCCA
93	T C ...	...	CCCTGTTCCTCATGCTGAOCTGTGTTTCTCCTCCCAAGTCATCTTCTCTGTTCACAGAGGTGGGCTGGAT GTCTCCCATCTCTGTCTCAACTTTAT[CT]GTGCACTGAGCTGCAACTTCT







68	G A	---	GCTAACACITTT TTAAACCGT	---	CATTTATTTTG AAAGCTATTCA GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCAGAGGGCTTGCTGGCTACTGG [G/A]TGTTAGTTGCAGTCTGTGTGCTCCCTCTCTTATGACTGTGTCCC
142	A G	CTC	GTATATTACA ATGATCACCG	---	COCCACAGAAC TATTGTAAAC AA	TTCTGAAAATATAACCCAGCATTGAGCTATTTAAACTGTAAATTTTAACTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAATAAACACATTAAATGCTAACACACTTTTAA ACCGTCTC[A/G]TGCTGAATAGCTTTCAAATAAATGTGAAATGGT
70	G A	ACTGA	---	---	---	TCACGTTTGGTCTCTCAGATTCTGAGGAAATGCTTTGTATTTGTATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTTCTGIGGGGCTGTTTTTTTGT
3b	314	C A	---	---	---	TTACAGAAACTTGCCCTGTGCCTGTGTCCCTCCATGCTAGGGCGGAGGGGCTTTTCCCTCTCTTTC TACCTACCCCTTTTCTTGGCCAGGGGCTGCTATCTCTACCTTTCTTGTCCCTGGCTGGCTGCAC AGAGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCITGGGAGGAACCATAGCTCCCT
3	96	G C	---	---	---	TTACAGAAACTTGCCCTGTGCCTGTGTCCCTCCATGCTAGGGCGGAGGGGCTTTTCCCTCTCTTTC TACCTACCCCTTTTCTTGGCCAGGG[G/C]CTCTGATCTCTACCTTTCTTGTCCCTGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCA CAAAGTCTAAGGGACCATGGCTGCCTGCCITGGGAGGAACCATAGCT
4	182	T A	---	---	---	CCCAGATGTCCTACACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACITTTGTTAAATATTTGAAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTGAAGAATATATGTT[A/C]AGAAACACAAAGGCTT GAT
3	78	C T	CTCTGCCA	CCAACAACAT CTCTGCCA	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTTCCCTTCTCTGCTTCTCTCTCATCATCATCCCAACAACAT CCTCTGCCA[C/T]ACACAACAACGTAAGTTTCATTGGGCAAA
6b	104	T A	---	---	---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGCTTCAACTCT TAAAGACATCTTAATCTGAATGTAAACAATTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTGAGTAATTCATCCTT
7	75	A G	---	---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTACATTTTGTATTAT GCTCTTA[G/T]GATTACAGACTGATGCCAGACAAACCTTGGGAAGA
10	79	T C	TGG	CTTTAGAAAA TCTGCTTTAAC	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGTGGCATCTGTGTTCTGATGCTTACTACATATGTGAACCACTACTTTAGAAAATCTG CTTTAACTTGGT[C/J]ATTCCTCTAATTGTTTCCCTAGGAAATGACTGTCCCAAG
23	107	T C	GTTC	TTGCTGGGCTGT GTTC	GGTCCAGAAGA GCGG	TGCTCCCTGTCCCATCTGCAGTGGACCCAGCCACCCCTTTGAGGAGGTGGGTGAAGTCTCCTT GGCAGGGATTGTGACACTGCATTGCTGGGCTGTTCCTCJCGGGCTTCTTGACCTTGACCCGTG GATACCAGGCCATGTGCCATGGTATTTGGGTCTTGGGAGGGTGGGTGAATAAAGGCATAGTGTCT

4	131	T A A A A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGAGGGAAGAGCAGAGTTAGAGAAAAAAGCCACCGGAGGAAAGG AAAAACATCGGCCAACCTAGAAACGTTTCATTGGTCATTCGAAGAGAGAGAGGAAAGAAAAA TT/AJACAACTTTCATTCTTTCGACGTTTCATAAACATCTACATA TCCTGCAAGAAGTTCCTCAAGCCTTTTGGATTTTGGCAATAAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTAAATTTTAAAGTGAGA/ACJCTCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAAATCTAAATATGTACCACCTGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATTTCA GTGCCACTACATGTTATAGAAACCATCATCTTGTCCACACAGCACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAAAAGTGCCCATTTAAAGGGACTTTTAAATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTTAAATACATGCTGAAAAAGGGTCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAT/AJTTTCAGAAC TACACAATGAATGCTTTTATTCGGTATGCATCCACATTCAGCATTTAGTGGTCTCTGAACAGCAAG TGGAAAGCAGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTTCGGGATCTGCTGTGCACACCGG GTTCTTCTTAATCCCTGCTGAGGATCTTG/AJGAAGCAGCAGCAGCACCCAAACCAAGGCATGCA CCGGATCAAGGTTCTTTTGTCCAGTTGTCCAGATTCCTCAAACTAGACCCCA AACAGTACACCAACACATGACAACTCGCCAGGAGGCTTGTCTCCCTCCCTCCCTTTCGCTCC ATGTGCTAGTCAGCAAGGTTCGGGAGGCAACCGATGTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAA/GCJGGAAAGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTGCTTTCAGTAACCTGGTATGCTGAA ACCAAGAGATCAGCTGTCTAACAGCAGCTTTTGTGTTG/TTGGGCTTCCTGAAAGAAACCTTGO TGACAGCTTCTCACTGACCTGCAGGAGGAAACCGTACCTGAGAGGGGATGGGGCTCTCTCACA GAATATTTGGGCAAGAACCTGGAACTGGCCACAGGACATCCCAATATCCCTCTCCTCAGGG CTCACCCGACATCCTCAGCCAAATGAAGGCTCTGAA GGGTGAGACGGGTTTATTTGTCACATTTACAGCGTCAACAGGCTCTGGGCTGGCAGCGCCATGCTC CTGTGGTGGGCTGCTCTACAAGGGGTTCACTTTCTTCCACCACTATGTACAGTCAGTGTCCAA GGTATGGGCTACAGTGTGATCAGTGTGTCACACACATTTTACATAAATACACACGACTC ATACATGAAAAIT/AJAGAGCCTAAGGGCTGTATTTTAAATGAGAAAAA AACTGTTTACAAAAATAGGCTTTCAAACCTTCACTAGTAATGTAAAGTCAATGACTGTGTTT TAAATATGTACCAAGGAAATACAAATTTGGATAATGATCATTTTTCAGTCTAGGAGAGAACAGCAC AGAAATAAAGGATACATGCACAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG G/AJGCACTTCTTCTACCTTAACTGCAGCTGTGCAAGATGCCTCAGTGTG
5	148	G C			
21	41	G T			
35	215	T A			
20	202	G A			

3	184	GA	---	---	TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGCTTGTGGTTCCAAAGGCTGAGAGCTGGACCAACG/AJCACTGGTTTCTAA TCTCTGGCTTGGATTTATCCAAAGCGCATGTTCTCAAGTGGCCCGTGAGCAG
3	204	GA	---	---	ATGTCAGAAGAGACACAGACAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGCAATATGATCTCCCTAAAGCCCCAGATTCCTACTAGAGCCGCTGGGGACACTGATGAC AA/GA/JGCAATCAACTCATCTCCTCAAGCTCACCGGGCTCACCTTCCCAAG
3b	201	GT	---	---	GATGATTCTGAAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGGCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGGTGGT TTATTAAATTTCAATTCATCTGACAGCCCTTCTTATAAGGTACATCCTTGCCCTCTTCTGAGGC/G TCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
3a	85	T	C	---	GATGATTCTGAAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGGCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGGT GGTTTATTAAATTTCAATTCATCTGACAGCCCTTCTTATAAGGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
1	149	GA	---	---	TTCAAGTGATAAGGACAGGCTAGAACAGCGTTCCCAACCCCTGGCACCATGACAGTTTGGACCAAA TAATCTTTTGTTCAGGGGACTGTCTACACATTTGGGATGTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA/GA/JCACAACACCCCTCCCCAACAAATCATGACAATGAAAATGCTTTAGACATT GCCAAATATACCTTGTGGACAAAATGGCCCTGATTGAGAACCACTGGTT
5	110	GA	---	---	AATGATCATTTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTTACATATGGTTCTTCCAGGAATCG/GA/JCAATGCTAATCTATTGCTTAA TTCCTTATCAAGAGACTCTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCTGAC CCCTGCTACGGGAACATTGAATGCA
3	199	T	G	---	ACCAACCGTTGGCAAGGCTCCCCAAGACTACCAACCCCACTTTGGTGCTTACCTATGCCGGGTG GGATTGAAGAAAATAACCAATAAATAAATTGCTACAAATTTTCCAGTAGTTACCAGGCACAGCCTAT TGAAGAAATCATAAATGTAAACCTACAATGATTGCTCTCTGGCTGGTGCCAGGCATAGAGTT/G JGGCTACAACCCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
1b	157	GA	---	---	TGGTATTTTCTTTCTTCTAAATGTTATGATTAAATAGTGCTTTGTAGAATTTGAAAAAATGTAAA TCAGAGAACAGAAAAAATAAAGTATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA/GA/JAGGGAATGAGAAAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAGTTAAGT

1a	48	A G ---	---	TGGTATTTTCCCTTCTAAATGTTATGATTAAATAGTGCTTTGTJAGJGAAATTTGAAAAATGT AAATCAGAGAACAGAAAGAAATAAAGTATAGTTGAAACCTCTAAACAATTTTAGATTTTAAAGGCC TAGGMAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAGCACAACCAAGAAAAAAGTGTGT GGCTAAGGGAAGCCAAAGGAAAGTTAAGT
6	61	C A ---	---	TTCTATTTAAATCCTGTGCCCATTCGAAGACTGCATTAGTCTGCATGAGCCTTAGTTTCJAJTAA AAGCCCCCTCACACCGAGGGACAATGTTCAAGAACTAAATGACTGCAGGTGAGCAATTTCTGTATTA TACAACTGGGACCAAGAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAAGTTATTTAACTT
1	153	C T ---	---	TATTACTAGGTTTATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCACGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGACTGTGTCTTCJGTTCCTGTTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
6	221	G A ---	---	AGAAGACAGGAGGACTGGGATCAAGGACTGATAAAGTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTTGGTATACCTTCTCTTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGAGTTTTCAGATGTGACTTCTACATCTCGAAACCTAGATGAGTTAGGCTCTCTTCACT CAATTGAAAATCTAGAAJGJAAAAACACCTAATTGGCTCATCTTGGATCA
0	49	C T ---	---	TTTTCGTTAAGTCTTGTGAAGCCACACAGAAAGTATCTACTCTCTTACJCTAAGTGTACTTTGCA TATATTTATGGGATGATTCTATCCCTACTTAAGATTTTCTCTCTCAGGTTAAATATCCATTTCT TTGTCAGGAGTTCTTATTTGGCCTCTTTCTAAACCTTAACCATCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
5	31	A C ---	---	GAAACCTCGTTGGCTCAAGGAAACTGTAGJACJAAATCTTTTTTTTATTTTGTCTTAACTC AAAGAGTGGAGTTTGACCTTGATGGCAGCCTGCTCTTTGTTTGGTAAATCCTCTAGT GGGCACCTTTCGAAAAGCAATTTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAG TAGCAATGGAAGAAAGGTTAATGGA
12	41	A G ---	---	AAGGCCAGTGGGAAAGCAGACAAAACACTCCAAGAAATACJAGJAGATATAAAACATCATCA GTAGAGATGGGATGACCTAGGAGGTATGCTGATGAGGGCATGTGACACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGTGCTTGCCAGTCCCATAGTAGGTTGCCATAAAATAAG AGTGACTAACTGAGGTAGAGTCACAGAAAGAAATTTCA
52	179	C T ---	---	GATTCCTTGGCAGATGCAGAGCAGATACGGCAAGGCATCTTGGGCAATTTGGAAGGAACGAGCCCTA ATTATAGAAACAGACTACAAAGGACCAGTTAAAGGTCTCGACACGAGGAGCTGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAGTGGGACAAAAGGCTTGTCAJCTGTGTGAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

167	A G ---	---	TGGTGAAGGCTGAAGGCTGAAGAATAGTCTCTGCTCTGGTCTTCGTTGGAATGGATGAGTCTCT TTTACAAAATTTTCTCTGCGCATGGGTGTTATGTTTGAATCAITGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGTA/GTGAACCTTGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
198	G A ---	---	GGTTTCATTTAACAGCCTTCCCACTGGGCTCAGATTGACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACACACATTAAACTCTCTCCCACTCTA CCGCGCAAGTCTACCTTTTGGTCTTTTATTTCTGCTAATGACCATACTATTTCCTCAATTAGA[G/A] CCATGTCATTTTCAGAAAAGAGTATA
184	C A ---	---	TTTATCTTTCCAAACCATGTGTGTTTCTTCACATACTTTACGTAATTTTAAATCATGTCAATTAATTA TGCACCTTACTTGTGGTACCAGACATTGCTTCCAAATTTGTAATTCCTTAACAACAGCAAGCATAACT GATGTCCATCTTTGTATTCTCTAAAC[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT CTTCCCTGTGTTCACTCCCTGTAATTCCTTATTCAGCAATTCATGATTA
72	A G ---	---	AAAAAACAACTTCATTTGACATTTCTAAGAGATAAGAAAACAAACGATCCACTGTGTGTTGCTT GATTTA/GGGAGATAAACCTGATCTCTAAGAAAATTAACCAAGCAGTACACTAAAATAGCCT TTGTGTGGTTTTCAGGAAGAAAAGCCAAATCCAATGCTAAGTAAAGTAAATATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAAATATAGCA
111	C A ---	---	TGAAGGACCATTCGAATGCCTACCAAGGTAAAGTAAATCGAGGGGCGAGGAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGTGC[C/A]AAAAATTTAACACTGATGC TGCTACAAACGACATAGAAATCGGTGGTAGATTGCGGTTCTTAGTAAGTAGCTAATGTTTAGATA TGATTTGAATTTGTTGCTGTGTTCTGGTG
177	A G ---	---	CAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTATGTAAGGTGGGCGAGGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAG/A/GTCTCTCCAAATTTACGGGGCTCCC GTGGGATGTTGGAGCCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
34	T G ---	---	GGGATTCATGTGTCTCTCATCAATAAGCACT/GCATGACCTCAGCCCCATACTCTTTCTCCC TATGTTCCAGAGACAGAATAGACTGGCCCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGGATCTTCTAGTTGA
88	T G ---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGGCTGCTTTCGTTAACTGTGTATGIACATA TATATATTTTAAATTTGATTT/GIAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAAGTT ATTTCTGTTTGTGTTGGGTATCTGCCAGTGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCATTTGTAATAAAGTATATAATTTTTTATGTTTGTCTCTGA

a	44	T C	---			GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGCT/CJTTCGTTAACTGTATGTAC ATATATATATTTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAAGTT ATTCTTGTGTTGTTGGTATCCTGCCAGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCAATTTGTAATAAGTATATAATTTTTTATGTTTTGTTCTGA
	197	T C	---			TCCAGAAATTTCTCTTCAGCTCAITTTGTCTCTCACAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCAITTAATTTCCCTTCAACAAATAATATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAGCCTACAACATTTTTT/CJAG TTTGCAATAGAACTAATACTGGTGAATAATTTACCTAAACCTGGTTATT
b	57	G A	---			AGCCAGCTGGACTGATGGATGTCACCCCTTGTCCCTGCTCTTTCTGCCCTGGG(GA)CTCATGTA TCTGGCAGCTGTGTAACCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTGGCTTGAAGCT GAGAAGGCACAGGCAAGGAGCCAAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAATCAGGGGGCTGCTACTAGAGCC
	69	G C	---			CTCTCTCTCATCCCATCACCCCTAAATAGGTCAAGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G/GC/JAGAAGTGAAGGAAGATAGGAAGGATATACCTCTCTGTTATTTTAAAGAAACATTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTAGAGGCTAAATTTATATCTATAAATATATAAAA AGCAAGTCAAACTTGGATGATCAAGGTAAATATTGTCAAAAGTTTAAAT
c	242	T C	---			GAAGGAGCTGGATCACTCCGCGAGTCTTGGCAGCGCTTGTGTGGACACAGAGACTCCTCCT CAGGGGCTGGCAGTCACTCACTCTATCTGTATGATGTTGGTTAACTGTCAATAATAGAGAT GTGCCAGATTAGATTTCTTACCCTAATCTGTTTAAATGTAACTTATCCATTTGAAAGTGICA AGCCCATTCAGATAAGCTAATACTGGTCTTTAAGGAAT/CJACAACTTT
	101	T G	---			CTCCCTCCTATGTCTCAGCAGCAGCTTGGGCGCACACTGTTCACTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTCAT/GJACAAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCAITTAATAAATACGTACATTTGAGGTAATGGTA
d	131	T A	---			TTTTGAGTCAAGAGACTTAAGGGCCCAATGAATTAATATACATACTGCATCTTGGTTATTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACACCCAAACACTTACACCAAAC(T/A) ACTGAATGAAGAAGTATTTGGTAACCGGCCATTTTGGTGGGAATCCAAAGATTGGTCTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
	99	T C	---			TACAGTTCCAGCCGTTGCCCACTCATCTGCGCGCTTGTCTTGGTTGGGGGCGAGATTGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTCATGT/CJAGCCCCAAAGTACAGCCTGGACCAACCTGGTGTG TGAGCTAGTAAGATTACCTGAGCTGAGCTGAGCCCTGAGCCAAATGGGACAGTTACACTTGACAGA CAAGATGGTGGAGATTGGCATGCCATTGMAACTAAGAGCTCTCAAGTCA





25	A G	---	---	AGCTTTTGAATCCAAAAACACATAGJCTTGACTCTCTTATCCTCCTCTGTTGTAACATCTATCC CTGAGGCAGAAATACAGAACACCCCTGTGGCTGCTGAACGGAGGAGGATGGGGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCGCTGAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCCTCCTGCTATCCCTGATGACTGGGCAAA
				TTTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAATTTAGAACTACTCCGJGJTTTT TTTCCCTGGGAAATATTCACAAAACATTTGTGCTGCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGICATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCATGCTGTGAGACTTTATGT ATTCAATTTAGAGCCAGGGCTTGTCTGTGACCCAGCTTTCAGTGAGT
59	G A	---	---	CTCTCACTCCAAACACTATATGCTTACTTAATGGTTACAGATTAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCATGCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
				CTCTTCACTCCAAACACTATATGCTTACTTAATGGTTACAGATTAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCATGCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
106	T C	---	---	CTCTTCACTCCAAACACTATATGCTTACTTAATGGTTACAGATTAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCATGCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
				CTCTTCACTCCAAACACTATATGCTTACTTAATGGTTACAGATTAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCATGCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
2	103	T C	---	GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATGJGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAT
				GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATGJGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAT
17c	141	A G	---	GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATGJGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAT
				GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATGJGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAT
17b	141	A G	---	GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATGJGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAT
				GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATGJGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAT
97	136	A G	---	TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAT
				TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAT

				TTCAAAITTAACACCATGGGTATATTATTAATTTINGCTCTATCCATAGTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCTTCTATTGTCTTGACGTATTAGGTATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCAITTTCTGCTGACCCCTCCCTCCTCACCCCTACTTGGCTGTGACTTCTCTTCTGGGCT GAACCTTCTCTGTGGCTGTCCGCTTCTCTCTGCTGGCTCAATAC
66	GC	---		TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGGTGCAGTATCTACCCCTTA GGGATATTGTGAGAAITCAATAAGTTTATACAGGGGAAGCACCTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTATACTATGGCACCAATTTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
b	156	AG	---	TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGGTGCAGTATCTACCCCTTA GGGATATTGTGAGAAITCAATAAGTTTATACAGGGGAAGCACCTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTATACTATGGCACCAATTTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
	156	AG	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCGJGJTTTGTGTTTGGC CAATAATATCTCCCGAGGACGTCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCACAAAGCACACATTAGAAACTTA
b	119	GA	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCGJGJTTTGTGTTTGGC CAATAATATCTCCCGAGGACGTCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCACAAAGCACACATTAGAAACTTA
	113	AG	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCGJGJTTTGTGTTTGGC CAATAATATCTCCCGAGGACGTCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCACAAAGCACACATTAGAAACTTA
	119	GA	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACGTATATGGCCTGAATTTGTATCCCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCJGTATTTGTACATAA
b	123	CG	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACGTATATGGCCTGAATTTGTATCCCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCJGTATTTGTACATAA
			---	TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCJGTATTTGTACATAA
			---	123 C G ---

198	T C ---	---	AGGTTCTGGACTTGATGCTGGGAACAATTGGTNCCTGAGAAATTCCTATTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAGGTATCCTAGTCCATCCCTTTATAGGAACCTTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCGGCATGCAACATTTATTCAGTGAAACATGATGAAATGAACATAAT
205	G A ---	---	CAC TTC AAGGGCTCTGGGGANGAGCGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTTACTGG CAGTGATGCCCTCTCACGCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGCAGCATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATCTTCCGAG
205	G A ---	---	CAC TTC AAGGGCTCTGGGGANGAGCGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTTACTGG CAGTGATGCCCTCTCACGCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGCAGCATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATCTTCCGAG
90	G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAGNA GAAAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
90	G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAGNA GAAAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
167	C T ---	---	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTACCC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[CT]CTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
155	G A ---	---	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTACCC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
181	T C ---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATATGATGTCCTAGGTACATTTGTTTTTTTGTCTG CGAATTTGTTATCTTTGGGAGAAATGCTCAACTATAAATATGCTTCTGACCCCTTTCTGTGTTG CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GGCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTATGCTCTGGCTTCATTTGTAAATNG

17b	204	GA	---	---	TTTGCCATTATTTGAAGATAACCCACACACCTTGGTGCTCCAGGGTTTCACAGGTTTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATCCAGCCACCGCAAACCTTCTCCTCCCTGCTGGCTC CTGAGCCCAAACAGAGGCAATTTACCATAAATCACCTTTGTTAGGATGAACCTTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATAGGCAGA
18b	147	CT	---	---	GCATTGAGAGGGTTGTTTAAATGACATTCACTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCTCCTGAGTGTCTGAATGCGCCAGGTGGC TAAGTGTGGGGC/GT/CTGGGGTCAGGCTGCGCTGGGTGCATCTGCTGGCTCCAAACTGCTTGTCTATG GCT
18a	124	CG	---	---	GCATTGAGAGGGTTGTTTAAATGACATTCACTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCTCCTGAGTGTCTGAATG/GIGCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCGCTGGGTGCATCTGCTGGCTCCAAACTGCTTGTCTATG GCT
14	124	TC	---	---	AAGTTTACAGAAAATAACAGAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGNCCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGN/T/CJGNCANT AAAAATGATTTGAAATTTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GCG
15d	202	CT	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
05c	46	CT	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
15b	153	TC	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/CJTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
05	202	CT	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

				TTTCTGCATTGGAATAGTTGACITCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCTGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGGAGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTGAGTGC
b 248 A G ---			---	TTTCTGCATTGGAATAGTTGACITCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCTGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGGAGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTGAGTGC
240 A G ---			---	TTTCTGCATTGGAATAGTTGACITCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCTGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGGAGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTGAGTGC
b 118 T C ---			---	GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTTCTCTCACTTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGGTGGGGAGCAGTGGGTAGGCAAT/CJGTGAGATTGCTTTT CCTACCCCTCTTAAATGTATCTTNCATTAATATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGTTGCTGTTGTTTCTCTCTGTAAGNTGTTT
118 T C ---			---	GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTTCTCTCACTTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGGTGGGGAGCAGTGGGTAGGCAAT/CJGTGAGATTGCTTTT CCTACCCCTCTTAAATGTATCTTNCATTAATATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGTTGCTGTTGTTTCTCTCTGTAAGNTGTTT
3b 169 T C ---			---	GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCTTTCCTCTCT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTAGGTT
5 165 C T ---			---	GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCTTTCCTCTCT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTAGGTT
7b 162 T C ---			---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAGCTGTGTAGTGCAGAAAGTCTGTTATTGTAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTACGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGT/CJGAAAGTGGGTAGTACCAGGCCTCCCCAAATGTAGT TCTTGNCGTGAAGTCTCTCTACTGAAGAGGCAATGGTTCCATCTCTAAG
7 175 C G ---			---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAGCTGTGTAGTGCAGAAAGTCTGTTATTGTAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTACGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTGGGTAGTACCAGGCCTCCCCAAATGTAGT TCTTGNCGTGAAGTCTCTCTACTGAAGAGGCAATGGTTCCATCTCTAAG

41b	136	GA	---			TATCAGCATGATTGGCTGTGGACACAAAGTCAATTTGACITTTTGNIGNNNTCTTTCTNTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCITTTGTTAAITATACCCAAGC [G/AGGATTGTGATGGATCTGTTTATTTTCTCTGTCTTGAACAGAGAGTCTCTGNGAGTNTG GTTTCAGGATTGTCTGTCTTCCAGGCCACTTGCACTTAGCAAGTGT
49e	192	GC	---			CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTAAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
149d	264	CA	---			CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTAAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
349c	192	GC	---			CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTAAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
349b	264	CA	---			CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTAAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
349	264	CA	---			CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTGAGTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTAAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
1403b	57	CT	---			TGGTATTGGAAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAAGTTG[C/TTCCGAA GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG AAAGTTTACATCAACATAATCTTGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT
1403	58	T C	---			TGGTATTGGAAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAAGTTG[C/TTCCGAA TGCACCTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATCTTGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT

c	31	C T	...				CAGCCGGAAGAGATCACGTGGAGAGATGTC/TJTTGGCCAGGGCGGCGAGATGTGAGCCACGGG GGTGACAGCATGCCCTGCTGGCAATTTGGAGGGCCCCAGAAAGAAATCCAGTGGCCCTCTCAATGACTTG GGTGCTCGACTCGGAAGTTTAAGGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGGGAGGCCCTTAGGTCGGTATTAAATGTTTGGTTGTAGAAAAGTGGC
b	31	C T	...				CAGCCGGAAGAGATCACGTGGAGAGATGTC/TJTTGGCCAGGGCGGCGAGATGTGAGCCACGGG GGTGACAGCATGCCCTGCTGGCAATTTGGAGGGCCCCAGAAAGAAATCCAGTGGCCCTCTCAATGACTTG GGTGCTCGACTCGGAAGTTTAAGGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGGGAGGCCCTTAGGTCGGTATTAAATGTTTGGTTGTAGAAAAGTGGC
							CCATGAGCAACAGCATGTTCTACTCTGTGATGTATGTTAGGGGCGATGTATCTGTATTTCTT TTTATTCTCTCCAAAAGAAATTTTCAATATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGATGTGCTCTCCGTGGTACCTTCTCTCCACCATCACCTGTGTTTT
	172	A	...				TGCCTTACTCTTGTTCATCCCACCATTACATTTGTAAATGGAACTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAGGGGACATATCAAGGAGTNCCTGGTCAAGCTTTT/CJATTGAGTCT CTGCCACATGCTAGTAAGTGTGATGGTGGTGCATCAGTATAATCCTGAGCTCCCAAGGTACAGC CTTTCACACTATTATCATATTTGGCTAAGGTATTCATCATATTGGCTAAG
2b	122	T C	...				TGCCTTACTCTTGTTCATCCCACCATTACATTTGTAAATGGAACTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAGGGGACATATCAAGGAGTNCCTGGTCAAGCTTTT/CJATTGAGTCT CTGCCACATGCTAGTAAGTGTGATGGTGGTGCATCAGTATAATCCTGAGCTCCCAAGGTACAGC CTTTCACACTATTATCATATTTGGCTAAGGTATTCATCATATTGGCTAAG
2	114	C T	...				GCGAAITTAATGACTCCAAAGGTAGTAATCCTTCCCCCAAAAAGGTTTAAAACTGTGTTGGA CATAATGTTTGAATTTGCAGTTACCTTGGAGTAAAGGTGTGCTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
0	97	A G	...				GGTACACAAAGAAATGCTTCTGGAAATCTACJAGTGGCCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAACATGAAGCTGGGCAAGAACAAATCTAGGAAAAGTACAATTAC TGGGAACTGTAGAACAAATATTCATAGTTTACACATAGCTGGGAATCAGTGTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATCAAGAAATATCAATAAAAT
10	31	A G	...				CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTTAGGCAATATAATATTTTTCAGGCAGAA CCATTATGATJAGTAGGTAGGATGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAATAATATCTACTAAAGCATGACTTCTAGAAAATTTACTTACTCTTGTCTCAA GGAATGGGAATACCTATAATACAGTCTTATGAGGAAAATAACTGGAATCA
33c	77	A G	...				

103b	77 A G ---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATAGJAGTAGGTAGAGCATCACACTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAAATTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATCTTGCTCTCAA GGAATGGGAATACCTATAATACAGCTTATTGAGGAAAATAACTGGAATCA
137b	112 C T ---	---	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC/C/TJCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTGAGCT CGTGTAACAACCTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGGCT
337	112 C T ---	---	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC/C/TJCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTGAGCT CGTGTAACAACCTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGGCT
340b	79 G T ---	---	TCACCTAGGGAGGTGCTAAAATGTAGCTTCATTAAAGACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGCT/G/JGAGAACTGTAATATTAGCAGACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTTACTAAAAGTTCCTAAAGCCATGAAGAAATTAAGACT ATCGCA
840	79 G T ---	---	TCACCTAGGGAGGTGCTAAAATGTAGCTTCATTAAAGACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGCT/G/JGAGAACTGTAATATTAGCAGACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTTACTAAAAGTTCCTAAAGCCATGAAGAAATTAAGACT ATCGCA
879b	110 C T ---	---	GGGCTCAGTTTCATCAGAGCACATATCAGTGATAGTGTCTTCTCTTTTCATTAAGTACTCCCCCG CACTGTAGGNTTCTTTTGGGTAAGGACCTGCCNTTTTTC/TJCTGTGCNAAATAAATCCCCAAA AAGTGTAGTCCACAGGGTTTAAATAGTTCTTGTGAATGAATTTCTGTGTGCGACCCCTGTGCCTCT CAAG/AAAAAAAACATTGAAAATCTCCACAGAGCCCTTTACCCACT
879	110 C T ---	---	GGGCTCAGTTTCATCAGAGCACATATCAGTGATAGTGTCTTCTCTTTTCATTAAGTACTCCCCCG CACTGTAGGNTTCTTTTGGGTAAGGACCTGCCNTTTTTC/TJCTGTGCNAAATAAATCCCCAAA AAGTGTAGTCCACAGGGTTTAAATAGTTCTTGTGAATGAATTTCTGTGTGCGACCCCTGTGCCTCT CAAGAAAAAAAACATTGAAAATCTCCACAGAGCCCTTTACCCACT
900b	119 C T ---	---	TGTTCTCTGGTCCAGGACCGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAAACCCNG CTNAGGTAGGNTTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG/C/TJGCTCTGAGAGGT AAAGTGCCTGCCCCAACCGGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAACCTGCCATGAGAAACCACTTTCTTTTGTCTC



					TGTTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCATAATGGAATATCAACTGGACAACCCCG
					CTNAGGTAGNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAAAGAGC/C/TGCTCTGAGAGGT
					AAAGTCCCTGCCCAACGGGCACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT
10	119	C T	---	---	GACTTCAGATCTGTGCTTAACCTGCATGAGAAACACATTTCTTGCTCC
					ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT
					GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC
					AGCAAGCCAATGGGTAGGGAAGACCAGCC/C/TCTCTGAANCTGGTCCACGCTGGAGATAGTGAA
13c	165	C T	---	---	TACAGGGCACCGNTGAGCATTCACAGTACTCCAAAGCCCGCTGGAGTAT
					ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT
					GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC
					AGCAAGCCAATGGGTAGGGAAGACCAGCC/C/TCTCTGAANCTGGTCCACGCTGGAGATAGTGAA
13b	165	C T	---	---	TACAGGGCACCGNTGAGCATTCACAGTACTCCAAAGCCCGCTGGAGTAT
					ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT
					GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC
					AGCAAGCCAATGGGTAGGGAAGACCAGCC/C/TCTCTGAANCTGGTCCACGCTGGAGATAGTGAA
43	164	C T	---	---	TACAGGGCACCGNTGAGCATTCACAGTACTCCAAAGCCCGCTGGAGTAT
					CCAGGTAGGGTGAAGAAAGGAGGAGGCAATTGCTGTGGAGTGAGGGATTCTGGAGAAGCACCCCT
					GCAGAGCTTCATCTGTTTTCAAAGGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG
					TTATCACAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA
60c	270	A T	---	---	GTTGCAATTAAATCCGTGGTGTCTGAAAACCTTAAAATGCACCTCCCAACTTT
					CCAGGTAGGGTGAAGAAAGGAGGAGGCAATTGCTGTGGAGTGAGGGATTCTGGAGAAGCACCCCT
					GCAGAGCTTCATCTGTTTTCAAAGGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG
					TTATCACAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA
160b	270	A T	---	---	GTTGCAATTAAATCCGTGGTGTCTGAAAACCTTAAAATGCACCTCCCAACTTT
					CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA
					TTCTGGGCATTTTCATAGAGTNTGTTTTCATGCTGCTGTAATACTGTTGCCCTAGGAAGTTGTT
					TTTCCCTACTGGCTGTGAAAGCCCTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTTT
177	203	T C	---	---	/C/TAAACAATCAACACTGGCTGAGGCTGTTGG
					AAATTCAGAGGCAAGTACGCTCAGCATTTATAAGTTGAAGTAAATGCATTGTAGTTTCATGT
					TTTCTCTTAATTCGCACAAAACCTAGCTAAAATC/C/TTAAATCAGTTACCAGAGGCAATACCT
					GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTGTGAGTCACTTTTTTCTACTCTCATT
112	102	T C	---	---	GGCTTCACCAATGCTTCCACTGGATC

3	127	C T	---	---	CTTTAGAGGTGGTCATTTCGGTTCCTCTGGAAAGTGATTGCTGTTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACTTC/CTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACCTGGAGGATATCTAGCTTCCTGAGCCCTGGTTACTGCAATCC
32c	166	G A	---	---	ACCAGACATCCCATCAGGAGTTAGTCTCTGGCAAGCCAGCCCTGCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACG/ATGTGGGACCTGTCTCAACCTCCGACTTTCACAG AGATCATTTGGTTAGGCTCACCTTCCTGTAATTGCTTCTGTTTTTCAAAGGG
32b	219	C G	---	---	ACCAGACATCCCATCAGGAGTTAGTCTCTGGCAAGCCAGCCCTGCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTTGGGACCTGTCTCAACCTCCGACTTTCACAGA TCATTTGGTTAGGCTCA/C/GCTTCTCTGTAATTGCTTCTGTTTTTCAAAGGG
32	219	C G	---	---	CGTTTCTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAGACAGGTGACCTTTCAAATAACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTTC/CTTCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
54b	188	C T	---	---	CGTTTCTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAGACAGGTGACCTTTCAAATAACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTTC/CTTCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
54	183	T C	---	---	TGGGATTAACACCTGTTTCTCTCCAGTTCAGTGTGCTTAATGTTGTGCTAGAAATTAAACA TTAAGCAGCAGTAAATAGCTCTTAAATGCACCTTCCCGTTCAAGGGTGTTCOGTGTTC/CTGA TATCATCTGATCTCCCAACAGGGCTTATTTATGCTAGGTAGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCAAGGTCATATGGCTGGGCTGGACGAG
73d	129	T C	---	---	TGGGATTAACACCTGTTTCTCTCCAGTTCAGTGTGCTTAATGTTGTGCTAGAAATTAAACA TTAAGCAGCAGTAAATAGCTCTTAAATGCACCTTCCCGTTCAAGGGTGTTCOGTGTTC/CTGA TATCATCTGATCTCCCAACAGGGCTTATTTATGCTAGGTAGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCAAGGTCATATGGCTGGGCTGGACGAG
73c	165	A C	---	---	TGAAGTGAATGATTTGCTTGCAAGGTCATATGGCTGGGCTGGACGAG

3d	129 T C ---	---	TGGGATTAAACCCCTGTTTCTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTTTCJTGGA TATCATCTGATCTTCCCAACCAGGGCTTATTTAIGCCTAGGTAAAGGGTAAGCAAAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCAACAGGTCATATGGCTGGGCTTGGACGAG
3c	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACCAGGGCTTATTTACJTGCTAGGTAAAGGGTAAGCAAAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGCAACAGGTCATATGGCTGGGCTTGGACGAG
3b	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTTTCJTGGA TATCATCTGATCTTCCCAACCAGGGCTTATTTAIGCCTAGGTAAAGGGTAAGCAAAACAGAGGCTGTGT TGAAGTGAATGATTTGCTTGCAACAGGTCATATGGCTGGGCTTGGACGAG
3a	129 T C ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAAGCAAGCTTCCJAGJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTACGGCTTCCCAATGATGCAGCCCACTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
38b	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAAGCAAGCTTCCJAGJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTACGGCTTCCCAATGATGCAGCCCACTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
68	60 A G ---	---	CATGCTGTGAACCTCTGTGCTGCTGTGCTGCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTCJ AGAAATGAATAGAGCCCCATTTTAAATATATACAGGCTTATGTCCACTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT
70b	131 T C ---	---	CATGCTGTGAACCTCTGTGCTGCTGTGCTGCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTCJ AGAAATGAATAGAGCCCCATTTTAAATATATACAGGCTTATGTCCACTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT
370	131 T C ---	---	CATGCTGTGAACCTCTGTGCTGCTGTGCTGCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTCJ AGAAATGAATAGAGCCCCATTTTAAATATATACAGGCTTATGTCCACTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT

14c	49 T A ---	---	TTAGCACATATCTGTTGGGACCTAACTGAGACAAGGCATAAAAAAT/A/CAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATTAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
34b	41 A G ---	---	TTAGCACATATCTGTTGGGACCTAACTGAGACAAGGC/A/GTAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATTAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
34a	38 G T ---	---	TTAGCACATATCTGTTGGGACCTAACTGAGACA/A/GTGCATAAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATTAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
71b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCATAAGCTTCTTTCAAACAATTTGTAACTCCTCCTCTCTTAATAAACCTTAAC ATTCTTTTGTCCCTGACATTCGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATTCTGAAGAAAACCTTTTACTTAGGGATTGTCT
71	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCATAAGCTTCTTTCAAACAATTTGTAACTCCTCCTCTCTTAATAAACCTTAAC ATTCTTTTGTCCCTGACATTCGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATTCTGAAGAAAACCTTTTACTTAGGGATTGTCT
195d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTTAA /TAAATCTTTCTCTGGT/G/CJTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
395c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTTAA AATCTTTCTCTCTGGT/G/CJTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAA AATGAGACAGAACTAGCAGAAAGTGT
395d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTTAA /TAAATCTTTCTCTGGT/G/CJTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

35c	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
35d	133	A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
35c	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
95b	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
95a	133	A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
47	85	C T	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGCTCCAGCTTGAGACCAC ATCTCACTTAGCTCCTT[C/C]CTGCCATATCCTGTTTTCCTTACTCTATCTCTGAGACTTCTTCTCT GAATGAATACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTNNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACCTTGGCAAGG
34b	68	T C	---	ATTCTGTAATGTTTTCAGTCTCCAGTAAATCTTATTGAGGTCCATGTCCATTACCTCTACTTA[ T/C]GACAAAGCAAGAACAAACAGAAAGCCCTGTTTGGCAATCTGGCTCTTATAAATACCTTCTG TATATTTTAAACAAGTACTGTAGAGTNAATGAATCATCATCTTAAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT
34	68	T C	---	ATTCTGTAATGTTTTCAGTCTCCAGTAAATCTTATTGAGGTCCATGTCCATTACCTCTACTTA[ T/C]GACAAAGCAAGAACAAACAGAAAGCCCTGTTTGGCAATCTGGCTCTTATAAATACCTTCTG TATATTTTAAACAAGTACTGTAGAGTNAATGAATCATCATCTTAAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT

92b	106	G A ---	---	GT TTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACCTCATCC TCCCTGTCCCGTCCCAAGCCTAIGTTACTGGIATGCTG[A]TGGTATGGATGGGATGGATTA GCCATGAATATTTTCCATTGTTTCATTAATGATTAATTAATTAAGTAAATATTTATTTNCCATGA GACACAATGGAAAATGGAAAACATTTCATGGAAAAAACCCATTTCATC
92	106	G A ---	---	GT TTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACCTCATCC TCCCTGTCCCGTCCCAAGCCTAIGTTACTGGIATGCTG[A]TGGTATGGATGGGATGGATTA GCCATGAATATTTTCCATTGTTTCATTAATGATTAATTAATTAAGTAAATATTTATTTNCCATGA GACACAATGGAAAATGGAAAACATTTCATGGAAAAAACCCATTTCATC
155	19	G C ---	---	CCATGAACCATGGGCTACA[G/C]ATATTCCTAAACTTCAGAGTCCCTTACTGGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATACATTTCCCAAGCACTTAAACATCATCAGAA AAAAAATCATCAAAAAGTCGAAAGTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACCTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
108	194	G A ---	---	CCATGAAGATGAGTTCCCTCCCTCCCTGGGTACGCTAAGAAATAGCACACCCCTTGAGAAATTTNACT TAGCACGTGGCATTGATGGCTGGATTCTCCGCTCTAAGACACACCTTTATGCTTTNAAAGCTTT CTGGATTGGGATGAATCTINACATTCATGTCACCTTCGTTGGGATCATTCTCC[G/A]TGCCCC ATCTCTGNAGAAGCCACTGGGAAAGTCGAAAGAGTGACTTCAATCAGG
305b	131	G A ---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAATTTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAAAC[G/A] AGGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANNGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
305	131	G A ---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAATTTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAAAC[G/A] AGGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANNGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
364b	177	C T ---	---	GCTAGTAAGTTCCACCTAAATGGTCCAAAGTCAGGAGAGTCACCTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTT[C/T]AACAAAGTGTGTTGGTGTGTCATC AGTGTACACATGCTACCTTCTTCCACAAAAACAAA
364	177	C T ---	---	GCTAGTAAGTTCCACCTAAATGGTCCAAAGTCAGGAGAGTCACCTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTT[C/T]AACAAAGTGTGTTGGTGTGTCATC AGTGTACACATGCTACCTTCTTCCACAAAAACAAA

[illegible]

					GAAAAATGATGTTTTGATTTCCCTTCCATCTTCAGATTATTGGAGTGTTCATTAGAAAACTGATAGT AACCTTTTATTGATGAAACTGTCTATAATTAAACCTTCTCTTCTGCTTTATTTTGGCTTC/CJACA GTTTAGGTAAATAAAGATGCCCAAGAAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAAGGGAGGAGGTTCTCTGGGAAGA
0	130	T C ---		---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAGAACAGACAGAGAAAGGGGT AGAGGAAGGAATCAGTTGTGTCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTCTTTCA TGAGACCGTCTGCAATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
9b	168	GA ---		---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAGAACAGACAGAGAAAGGGGT AGAGGAAGGAATCAGTTGTGTCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTCTTTCA TGAGACCGTCTGCAATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
9	168	GA ---		---	CAAGTCAGATTTTGATTTCAGGATAACAAATTTGAAAAATAGAAAAAGTG[T/G]TTTAAACTATTT CAATAAACATAAAGAAAAACATGATGAAATTCCTCGTTACATAATTGTATAGAAATTTAGTGGG TTCTCCATGACATTTGGCTTGTCTCTCAACAGTGGTGGTGGATGTTTCCATGCTTCTC AGGCACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
3b	51	T G ---		---	CAAGTCAGATTTTGATTTCAGGATAACAAATTTGAAAAATAGAAAAAGTG[T/G]TTTAAACTATTT CAATAAACATAAAGAAAAACATGATGAAATTCCTCGTTACATAATTGTATAGAAATTTAGTGGG TTCTCCATGACATTTGGCTTGTCTCTCAACAGTGGTGGTGGATGTTTCCATGCTTCTC AGGCACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
3	51	T G ---		---	TTGTACATGTTCAATTCATCCCTCCCATCTTTCTGTCTTATAAAGAACCTCGCTTCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTTATTTCCATCAAGCTTCTCAGCATCTTCTATATAC GTGCTGT[G/C]CCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTAACGTAGT AGGACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
9b	145	G C ---		---	TTGTACATGTTCAATTCATCCCTCCCATCTTTCTGTCTTATAAAGAACCTCGCTTCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTTATTTCCATCAAGCTTCTCAGCATCTTCTATATAC TICGTGCTGTGCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTAACGTAGT TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
9a	137	T C ---		---	TAACACACTTTTCATTTGGTTTCTTACTGCAGTTAAAGGACCATCCATTATATACAAATCCCTC AGTTCTATGCTTTAGAGTNCATATATAGGACTACTGTAAATTTTCAGAGGGAATTAATCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCAGAGGACTGTGGTTAA[G/A]ATGTCTCTCT TGCCCCCTTCCCAAGTCTTAAATTCCTAG
82	188	GA ---		---	



					AGAGACGTTGAATGGGACATCTTTCTATTTGATTTTGAATTTTAAACATTTGATAAGAAATGATGAAA GTTTGTACATCCAGATTATCTTTATAGCAGAGAAGTCTGGCAATAATAACAGCACACTGACT TTTCCATGGTAAAGAAGTTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATTTCTGAAT ACATTTTAAATGGAGGAGAAATGATGACCTTTGAAATTTTGAATTTATGG
10	93	T	---	---	GAAAATCCATTGAAGTTTTGACCTTGAACCTGATCTCATTAATACTTTTNCCTGAGTGTGTTATTT CATTTTGGACACAGACAGCAAAATTTCCACITTAATAATTAATTTCTC/TAAAGTATCTATGAT TTAGCACTGTTAGCACCAGAACTGTGAAATTTATCTCTAGATATTCTTCAGAACTCTAGGATGGAAG AA
11	118	C	T	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAAATAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTAGGAGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTAGAAAGTCCAGTCAGGGGC
71b	151	A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAAATAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTAGGAGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTAGAAAGTCCAGTCAGGGGC
71	151	A	---	---	AATCGAAACATTGATTTTTTTGTAAGGAACCACTATTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAGATAGAAAGGATATTATTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA/GI/ITNGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
89b	156	G	A	---	AATCGAAACATTGATTTTTTTGTAAGGAACCACTATTATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAGATAGAAAGGATATTATTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA/GI/ITNGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
89	156	G	A	---	GATGACAAATATTGTGATTGGCATTTTAA/GI/GTACCATTCCATTTTCTCTGGCTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGTTAGTCGTATTGCTCTTTTCTAGTCTTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAGAAACATAAATCAAAATTG TATTATCTCTATGCTTAAATGCTCAG
188	31	A	G	---	ACCATCAATGTATCACCTCTAAATTTATTAGATGATTAACCTGGCTCTGTTAAAAAATAAAAAACCT GTCTTGGACATTGAAAAATAAAGATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACCTA AACAAAGTTAAG/GI/GTTTTTGGAGGGGAAAAAATCATAAAAATGCATAAAATTTCTACCACCTGTCA TTTCTGTCCCCATAAATAAAATTTTACATGCTCT
191	145	G	C	---	

84	144	A G ---	TTGGTTGGCATTTTAGCCTCATAAACAATTTTACAATCAATAATTGTTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCACACTCTGCTTAGTCGAGAGCAAGATTTGAACCCAGGAATCCATT CACCGGTAC/GJTGCTACCTGGTAAAAAATGTTTAAATTAATCTATGGCATTAGATTTTCAAAGA GTCTAATGTGGTTTGAAATAGGTGCTTTAATTGTTTATCAGTATGC
39	185	C T ---	TTTTCGCAATTTGAATGTGATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTATTTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAITCCACCATTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGCTGTATCC/CJTCATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
127	63	A ---	AAATGAATCCGCTTTAGAGCAAATACCAGTAAGGCTGGTGAGGATGGTGGCTGAGAGA/- JGATTACTCATAAAGCATAATTAATTTTATAAATATGGAAATTTAATAGATAAATTAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGAGGAGGTAGTTCTTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAAATGGCTCTTTGGGATGACAAATGATGAATGTTCTAAGCAGACAG
390	87	C T ---	GCCTTTGAGAAATGAAAGGGAGCCTGGACCATTGACGGGCTTCTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTTAT/CJTGCTGCTCCCTCTGGTATGCTTGTCATGAACAATGAATTC CCAGTGCCTGGCCGATCGTGGCTCTAGAGGTGCCAGAAAAAAGTTTCGGTGAATAGAAATTG ACGAATGGGTTGAGAAATGAACTGTGAATCTATGGAAGACAAACGAAT
404b	87	G A ---	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAGAAATCAATTTAAGCAGT GCAACATTATTTTAAATTT/GJAAAGAAACTTGTTCGAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGTGTAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
404	87	G A ---	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAGAAATCAATTTAAGCAGT GCAACATTATTTTAAATTT/GJAAAGAAACTTGTTCGAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGTGTAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
545b	77	A C ---	TAGGAAAGGGATGGTGATGGCTCTGAGACATTTAAATCTATTTTACCACCTCACACTGCCGCCA TATCTCCTC/A/CJCCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTAAAGATTTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA
5545	77	A C ---	TAGGAAAGGGATGGTGATGGCTCTGAGACATTTAAATCTATTTTACCACCTCACACTGCCGCCA TATCTCCTC/A/CJCCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTAAAGATTTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA

				ACTCAAGTTGGGGATAAAATCAGAAAGTTCTCTATGTACAACCTTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGAATTTGTTTACTTCCCTAACCAACCTCTTAAGGAACTACAT GTTTACTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
860b	134 A G	---	---	ACTCAAGTTGGGGATAAAATCAGAAAGTTCTCTATGTACAACCTTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGAATTTGTTTACTTCCCTAACCAACCTCTTAAGGAACTACAT GTTTACTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
860	134 A G	---	---	GCAAACAACCTATTATACCTGATTCACACCCAGGTCTACTAACATTAACTAACCTAACCAATAC TATATATTGCTCTGTTCTGAATTTTTCATTTAGAACTCTGATGAGATTTAGCATGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGCCTCCAGGAGTCTCAATGTGAAGTATAATTCTTACAGAG TAATTTCGATAGTAGGTCACCAACAGTCTATTTGATGTGAAGGAAAG
3106	208 C G	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTTC AAACCTATATTNCTGTCCTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT GNAATAATTCCCTGAAATTTTATACCA
6109d	129 T C	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCTATATTNCTGTCCTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT TGNAATAATTCCCTGAAATTTTATACCA
-6109c	147 T C	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCTATATTNCTGTCCTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT TGNAATAATTCCCTGAAATTTTATACCA
-6109b	147 T C	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTTC AAACCTATATTNCTGTCCTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT GNAATAATTCCCTGAAATTTTATACCA
-6109a	129 T C	---	---	AATGCCTATACCTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAAACACATGCTGTTTGTTCATGATTCGCATATCCCAAGTGCCTTAGACAAATGCCCTCCCATAC AGTGAACAGATTTGACTAAACATACCTTGTTAAATCAATAAATAATTAACAACCTTGGCATATGCAGG GMC
I-6112	96 T C	---	---	

44	103	T C	---	---	TAATTGCACAACTTACATATCAGGGTTCTGATTGAAAGGAAGAATAATTCCTTTCTTTAGTGATT GCTTAATATAATTAATCATAAATAAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTAGAAAGAGG AAATTGAGTGTGGGAATTAAAGCAACGAGGAGACATTTTATATACTCTACAGTGGGGGAAGACTT CCTATTCTCTTCCCAAGGATGATACATTCTAC
68	124	C T	---	---	CTGGCCTTATAATCCAAAGTTAGGATTAACTTACCCCACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAGATTCTCTCTAGTAGGGCTTGGGTGTGGCACCGTTGGCTCAATCTCTCTCTCCCT GGGTCTTATTGACTTTACGGGAGCCTAGAAGAGCTGGACAAAACCTGCTTCTTTCAGAAAAGAGTCG GGGTCCAAAAGATTCTGATTCTTAA
136b	234	C T	---	---	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATATACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCCCTTGGAGGACACTGACAGT
336	234	C T	---	---	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATATACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCCCTTGGAGGACACTGACAGT
381	92	C A	---	---	TTGGATACAAAAATTCAGTTACAAATCAGTACAGTCAAAATAGTTATGAGTATTATACAAATTA CAAAAATGGNTTCATGTTTAAACAACAACTTAAAGCTCAACATTTTAAACAGGCACAAAT ATTCTAANGGCATATGCATTCACCATGGCTTTGAATGCTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAG
436	198	C G	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTTGAGGAGTAGAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGCATAATAAGAAGTTAGACTTTGGTGGTTGTAGTAGTTGTAGTAGGAGGTTCTC GATTGGGTGATTCACAGACAGAGGTGATGTTCTAAGATTGATATTATTGT
449	186	C T	---	---	GAGGCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTGGTGTCTCAGCTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTCTATTCATCTGCAATCTCTGATCTATGTCTGGCTCTATTCCTATCTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAATTTTCTGTGGTATTATA
449	186	C T	---	---	GAGGCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTGGTGTCTCAGCTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTCTATTCATCTGCAATCTCTGATCTATGTCTGGCTCTATTCCTATCTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAATTTTCTGTGGTATTATA

63	72 T C ---	---	GCTGGAGAGAAAAGACCTCCAAAAGAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACA[T/C]TGAATAAATTTAAAGTAGAACTCAAGAGAGCCAAAAGTCCCAATTTGTGTCATT TAAGAAATATTTTGAATGGAATCTTAAAGATGATTTTATGATCAGTTAAATGTTCTTCCTCTCCTC CAGTCCCATTATATGACATTCGGCATGCTG
174b	76 C T ---	---	AAGCAGTAATCTTCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAC[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAGCCATACTTAGGGTACCATAA
474	76 C T ---	---	AAGCAGTAATCTTCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAC[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAGCCATACTTAGGGTACCATAA
478b	175 T A ---	---	GAACCTCAATTAACCTTTCACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
478	175 T A ---	---	GAACCTCAATTAACCTTTCACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
3559	149 G A ---	---	CACATTTGAATGCAACTGAGAAANTGGTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCCA TTAGCAATATCTTA[G/A]TCAAAATTTTAAAGAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAANTAAATTTGTGCAAAACTTATCAGTCTTC
3564b	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTTCAGAAATGAAGGCATTTGATTATNATTTTTTTGGTCTGTGTAAG GTTCTCTGGCAGGAGAACATGCATATGACTTTTAAATTAAGACCAACA
6564	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTTCAGAAATGAAGGCATTTGATTATNATTTTTTTGGTCTGTGTAAG GTTCTCTGGCAGGAGAACATGCATATGACTTTTAAATTAAGACCAACA

08b	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAAGTGGGCTCAGT[C/- JAGTTCAGGAGCTAAGGGAGGGGATTCCTCTAGTCTCTCCTAGAGCTAAATATGCATCTGG GAAAATTAGGCTCTGGAGCACAGAGGTAATTTCTAGAGGAAAGAACTGAACTCCAGCACTAG GTAAACTGCAAAAAGAAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACAGAAAAGGAA AGC
08	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAAGTGGGCTCAGT[C/- JAGTTCAGGAGCTAAGGGAGGGGATTCCTCTAGTCTCTCCTAGAGCTAAATATGCATCTGG GAAAATTAGGCTCTGGAGCACAGAGGTAATTTCTAGAGGAAAGAACTGAACTCCAGCACTAG GTAAACTGCAAAAAGAAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACAGAAAAGGAA AGC
166	68 C	---	---	GTTAGACAGTATCCAGCAAAAAGGTTATTTATACCTCTACTTTCCAAAACGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGCTTACTCTGTTGTTTCATGTAA ATGTTGGGGTGAATCTCCGCTCTCTCTCTCAAGTCCAGGCTCTTGGGTAGACCAAACTA ATACAAATGTTAGAGCACACAGAGA
370b	120 A	G	---	AGATTACATAATTTACTGGGGCATTTAGGGTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAAATGAAC[A/G]TTGTAGCCA GCATTGCCATTTCAGGGCCGAGTCAGGGTTTGTGGGCCAGAAATTTAGACAATTTGGGGAATTCGA AAAAAAAAGAAATACAGAAATTGTAACACACAGACACAGAAATCTTAGAAGGGAT AGATTACATAATTTACTGGGGCATTTAGGGTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAAATGAAC[A/G]TTGTAGCCA GCATTGCCATTTCAGGGCCGAGTCAGGGTTTGTGGGCCAGAAATTTAGACAATTTGGGGAATTCGA AAAAAAAAGAAATACAGAAATTGTAACACACAGACACAGAAATCTTAGAAGGGAT TTTGAAATAAATTCATGCACCAATGTTTAACT[C/C]ACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATTAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCAIGAAGAGTCTAGTACAAGATAGGCAGACATG
704c	33 T	C	---	TTTGAAATAAATTCATGCACCAATGTTTAACT[C/C]ACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATTAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCAIGAAGAGTCTAGTACAAGATAGGCAGACATG
704b	33 T	C	---	TTTGAAATAAATTCATGCACCAATGTTTAACT[C/C]AACTACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATTAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCAIGAAGAGTCTAGTACAAGATAGGCAGACATG
3704	28 T	C	---	TTTGAAATAAATTCATGCACCAATGTTTAACT[C/C]AACTACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATTAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCAIGAAGAGTCTAGTACAAGATAGGCAGACATG

10	106 GA ---	---	COATGGACAGTTTAAITAGGAAGCTTCGACTTGTTAGAAATAACAGAGGAAGTCCAGTTATCTACCT ATTCTTTAAACACATTTTGTAGGCTGGAATGATTCGCCGAGTAGTAAACCTCAACATCCACACCT GCATAAACATCGCCTCCCAAGTGACTATTTACTAGTGACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAAATGGAGGAGTTGACTTAGACCTTCTTGGACAGGAAGGGTC
66b	148 GC ---	---	AAAAAAATGGTGCAATAATTTGGGTCACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAATCCAGTCCCTCTCTC
66	148 GC ---	---	AAAAAAATGGTGCAATAATTTGGGTCACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAATCCAGTCCCTCTCTC
787b	97 A G ---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAATTTTAC[G/C]TTTACTGCATAAGATATCTTCATGTACAACGTGT ATGCTTTGTCTCTTGGGAAGGACGCGTTAAAGACCTATGATAACACACATCCACATGACAAAAGGA GAGTGAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
793	105 CG ---	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATATGATAGCAAGTTTCAACACATTCA TCAACAAGGGCGTCTTCAATCAATCAGTCAACCCCG[C/G]GAGTTAGAAAGTAGATCATGAGGAA GAGCTGCTGGCTGTAGGAAGTAGGGTTAATGCCCTCTAATCCCGGAAAGGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAGGCAAC
3810b	37 T C ---	---	CACAATAATAAAATCACTCCCTACCTTGAAACCTTTAT[C/G]AGAAGCATTTTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACNGCCCAAGGATAAGGCTGAACAATA AATTAACCTTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
3810	37 T C ---	---	CACAATAATAAAATCACTCCCTACCTTGAAACCTTTAT[C/G]AGAAGCATTTTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACNGCCCAAGGATAAGGCTGAACAATA AATTAACCTTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
6817b	145 CA ---	---	GCATGATTAAACCAGTGCAGAAAATACCAAGTACATTTGGGTGAACGATGAGTGTCTTAGTA TTTGTCTTTTGTATCCAGTTAAGACCATCAGCATATACACATCATCACTAACAATGTAGCT GCAGGGTAAAC[C/A]TGTGGATACCCCTGTGTGCTCTACTNGCCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTTCAATCTTGGTTCAGGTGCGGCTGTGCGAG

317	145 C A ---	---	GGATGATTAACACAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTATCCAGTTAAGACCATCAGCATATACAAATCATCACTAACTCAACAATGTAGCTT GCAGGGTAAC(C)A/TGTGGATACCCGTGTGCTCTACTNGCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAACTTGGTTCAGGTGCGGCCTGTGCAG
319b	221 C ---	---	GATGGAAGGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTGCATATACAAAATTTCTGCTATTTTG CTTAGCAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCAG
819a	175 GT ---	---	GATGGAAGGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTGCATATACAAAATTTCTGCTATTT TTGCTTAGCAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATAT
826b	154 A G ---	---	GCAAAAGCTTTATTGGCTCCAACAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT(A)G/GAGCTTAAATAATATCAAAATGCAATATAGATTGGTGCAGTGT TAAGCTGAATTGCAATATTGGCAACACACACTGGACTGGGTATACGTTG
3826	154 A G ---	---	GCAAAAGCTTTATTGGCTCCAACAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTTGCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT(A)G/GAGCTTAAATAATATCAAAATGCAATATAGATTGGTGCAGTGT TAAGCTGAATTGCAATATTGGCAACACACACTGGACTGGGTATACGTTG
6857a	122 T C ---	---	AGTGCAAACTATTTTGAACAAAGTAACTATGAGTCACAGCATTGAGCAAGACATCAGACACGGA AGAGTGAACAAATATTCACCTAAGTAAATACAGCAGATGAGATGCTCTCAGATGTA(T)C/JATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTCAGTGTAAATTCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAAATGGCAAGTTTGGCAACTGTTTGGGCTAATT
6865	153 G A ---	---	TTATAGAATACTTATGGGGCATACNGTAAATGAACCTGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTGGTTCGTCTGAAATCCTCCCTGCTCACAACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTGTCAGGCAACTT(C)A/TAGAGCCATTCGTGCAGAGGAAGGGAAGGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGGGCTGTAGAACTGAGCTCATTA
-6909	73 C T ---	---	ATTGAAACTGGTTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAATGAGAGAAGATGC AGACTT(A)C/TJAAGCTTATAGAGAAAGTCAAAAGGAGCAAGTTTTTGAATCAGATTTTATGATAC GGAAAAAAATTCCTTTTTTGGCAACAGGATTATTCGAATAATAATCTGCCAGTGGCAATCAG AAACACCATTTCCACAATATTGTCATGCCCTAGTTGCTTATTTATACATATC



310b	163 G T ---	---	---	CACTCAAAACCCTTTATTCATTGATTTACAAACTGTACAAATATTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGGAGAGCTAAATAATAATATGTGGCACAATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAAATTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAAGTCCCGGACCTTCCATGTGAATGACTCTTCCTTGGC
915	144 A ---	---	---	GCCTGTTTTTTTGTGTTTTTAAGTGACACCTTGGCCTTGTGGCAATTTCTCACTTATCTTACCC AAAAGTGCCTTTGGGCCAGCCACTGACTGATTTAAACCAGAAATGGGTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTNAATTTCTATTTGGTAGTATTTTCAGATTTCCCAACAAAGAACATG TATTGCTTTTGTAAATTTGAAAAAATAATCAACACAGGATAGTAAAGATAT
928b	175 T C ---	---	---	CAATCAAAAAGTTCCAAGTTCAAAGCTGGGATGAAAGCCAGGCTTCTGACTTGCACCTCTGTAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCTCATG CTTTGCTTGGTCCCTGTGAGAAAGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
3928	175 T C ---	---	---	CAATCAAAAAGTTCCAAGTTCAAAGCTGGGATGAAAGCCAGGCTTCTGACTTGCACCTCTGTAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCTCATG CTTTGCTTGGTCCCTGTGAGAAAGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
6955b	79 G A ---	---	---	TTTTATGAACAATTCAGATTCCTCATATCAGCAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAAACTATAGGTAGTATATTAAACAAATGNGTTTTTNGCAAATTTATGTGAAT AAGGCTTTAACCAAAGC
-6955	79 G A ---	---	---	TTTTATGAACAATTCAGATTCCTCATATCAGCAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAAACTATAGGTAGTATATTAAACAAATGNGTTTTTNGCAAATTTATGTGAAT AAGGCTTTAACCAAAGC
-6957	47 C G ---	---	---	AAACTAAAAACCCTTATTGTCTCCAAGTGTGGCAAAATAGAAAAT[C/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATCCACTTAAGAAGCATTCAGTCAAAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTGGTCATTTATGGCTTGAAGAAGTGGATTGAAACCACCTTTAGG CTAAATAAATGTATATGAATAATGCATAGACTGTATCTAGAAAATCATGC
1-6996c	242 G T ---	---	---	ACTTCTAGTGCCTCTGTTACCAACCCTCTAATGCCCTCTGGTCGCCGACTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGCTTCAGCACCCAGAGAGGAGAGAGCGCGGAGTTCCCTG CAGGAGAGAGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTGCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCTCC[G/T]GTGGGATC

996b	242 G T	---	---	ACTTAGTGCCTCTGTTAGCACACACCTCTAATGCCTGGTGGCGGACCTCTGATGTCGTTAGGCTTAAATCTGCCTGGGTCCTCCCTCCCTCTGCTTCAGCACCGAGGAGGAGCGCGCAGTTCCCTGTCAGGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTGCTCTCAGGACCCCTGTCCTGACTCTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTTCGCGTGGGATC
996	228 T G	---	---	ACTTAGTGCCTCTGTTACCACACCTCTAATGCCTCTGCTGGTGGCGGACCTCTGATGTCGTTAGGCTTAAATCTGCCTGGGTCCTCCCTCCCTCTGCTTCAGCACCGAGGAGGAGCGCGCAGTTCCCTGTCAGGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTGCTCTCAGGACCCCTGTCCTGACTCTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTTCGCGTGGGATC
7021b	112 G A	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTCTGAAGCTCCCTGCTCTGAAAGCCACAGACAATATGTTCCCAAATGAGTCCGACTGCACTCTCTGTGCTTCAGCTCTTTCGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAAATCAATTAATCAAACTCTGTTATTAACAGATAATAGCAACTTGGGAATGCTTATGTTACAGGTTA
7021	108 A G	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTCTGAAGCTCCCTGCTCTGAAAGCCACAGACAATATGTTCCCAAATGAGTCCGACTGCACTCTCTGTGCTTCAGCTCTTTCGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAAATCAATTAATCAAACTCTGTTATTAACAGATAATAGCAACTTGGGAATGCTTATGTTACAGGTTA
7056c	118 C T	---	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGACCTTGGAGAGCCTGCATCCACAGGATGCGGGTGGCCCTGCAGGCTCCTCCACCTCACTCCATGACAGCGCTAAACGTTGGTGA[CTGGTGGGAGCCCTCTGGGCTGTGAAGTCACTTGTGTTCAGGTTCCAAACACAGAAAGTCATTCCTCTCTTTTAAATGTTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTGGCCATTGATA
7056b	118 C T	---	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGACCTTGGAGAGCCTGCATCCACAGGATGCGGGTGGCCCTGCAGGCTCCTCCACCTCACTCCATGACAGCGCTAAACGTTGGTGA[CTGGTGGGAGCCCTCTGGGCTGTGAAGTCACTTGTGTTCAGGTTCCAAACACAGAAAGTCATTCCTCTCTTTTAAATGTTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTGGCCATTGATA
7091b	153 A C	---	---	AATTCGCTGAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCCTCTTAACATCTTAGAGGTCCATGGAGAAAGGCATATGGAGAACATGTTTATACCTCTCTAATAAGTATTTCCAACTCACTGTGCTTAATTTAAATAGCATTC[CTCTATCAATATCAGCCCTTTATGTTATTTCCAAAGTAAATATTAACATATTTTCATTTGGTCTCTTTTTATCTGTTCTATATGAATGCTAT
7091	153 A C	---	---	AATTCGCTGAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCCTCTTAACATCTTAGAGGTCCATGGAGAAAGGCATATGGAGAACATGTTTATACCTCTCTAATAAGTATTTCCAACTCACTGTGCTTAATTTAAATAGCATTC[CTCTATCAATATCAGCCCTTTATGTTATTTCCAAAGTAAATATTAACATATTTTCATTTGGTCTCTTTTTATCTGTTCTATATGAATGCTAT

36	58 T C ---			TGTGAAGCCACATTTTCCAACTGAGCCTCATGAAGCCAACTAAGTGTATTGAAGCTGTC/AATTCTCTCAATAACTCAGTGTAGCACTTTAAAGTCTGAAGGACAGCAACATGAAAGAGCATATCAATGTGTGGAGAAAGGGAAGGGTGGCTTTTAAATTTATTTTCTTCATCTTTATAACAAGAAAGNNNGTAGCTTCTCTATATATG
46c	210 A G ---			GGGACGCCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTTGTTTGTAGCTGAATAATGAGTTGTTCTAGAGGACAGCCTGCTCTCTCTGTTGCCCCAAAGCCCCATGCCCTGCCGTGGTGGCAGCTGGGCTGTGGATGGGAGGGTCCCAACATGATGTGTGCCCTCTCTCCGATGOC AACGC[A/G]GTTTCATGTACAAAGCCCCCTCTGCAACTGGAGAGAAATTA
46b	210 A G ---			GGGACGCCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTTGTTTGTAGCTGAATAATGAGTTGTTCTAGAGGACAGCCTGCTCTCTCTGTTGCCCCAAAGCCCCATGCCCTGCCGTGGTGGCAGCTGGGCTGTGGATGGGAGGGTCCCAACATGATGTGTGCCCTCTCTCCGATG/A
146	202 G A ---			AACGC[A/G]GTTTCATGTACAAAGCCCCCTCTGCAACTGGAGAGAAATTA JCCAACGCAGTTCATGTACAAAGCCCCCTCTGCAACTGGAGAGAAATTA
153	161 A T ---			ATATTACAACTTGCTTTTGTAGTATCTCCATCCTCAATGACTCTTTTCTTTTATATGTTAACATA TATAAATGGCAACTGATAGTCAATTTGATTTTATTCAGGAACATCTGAAATCTGTCAGAGCCT ATGTGCATAGATGAAACNNNNNNN/A/TJAAAAAAGTTATTTAACAGTAATCTATTTACTAATTTAT AGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAATGGTATGTTT
155	156 T G ---			TAGAATAGATGGGTCATATCTCTTTGGCTTCTGGTTCTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAAACACAGCTGGCCCTACCCCTATAATGATCCTGTGTCCTAAATTAATACAC CAGTGGTTCTCTCCCTGT/GTJAAAGACTAATGCTCAGATGCTGTTTACGGATATTTATATTCTAG TCTCACTCTGTGCCACCCCTCTCTCTCCCATTCCTCCAACTCCAG
169b	161 A G ---			AGCTCCACCATGACAGATTTGTTTGTGTTTCTTGTATCACTGTCACACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGTAGCCCAAGCCATCAAGTGTCTGAAATCAATATGGTTTATGCAAAAT ACAGCAAACTTTTATTAAGTAGAT[A/G]GGAGAAATATGTTTAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATTCCTCAATGGAAAGTTATATA
7175b	194 C T ---			CTCCTAGACTAGTGTCTTACCTTTATTAATGAAGTGTGACAGGAAGCCCAAGGCAGTGTCTCCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATAATATGTTTACTGCTGCTATTGTCATGCCTA[C/T]AGAT AATTATTTTGATTTTGAATAAAAAACATTTGTACATTCCTGATCTGAGG

75	194	C T ---	---	CTCCTAGACTAGTGTACCTTTATTAATGAACGTGTGACAGGAGCCCAAGGCAGTGTCTCTCACCA ATACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAATGGTTTACTGCTGTCAATTGTCCATGCCTA[CT]TAGAT AATTTATTTTGTATTTTGAATAAAACATTTGTACATTCCTGATACTGGG
78b	273	G A ---	---	TGATCAGGTACGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGGCTCTAGGGGAACAGACCAGTACCCCAGAAAAGCATACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAGAACTACCC CCTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
78	273	G A ---	---	TGATCAGGTACGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGGCTCTAGGGGAACAGACCAGTACCCCAGAAAAGCATACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAGAACTACCC CCTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
182b	116	A C ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCT[AC]TCTCTCCTCCTATTT TACTTGAAGCTGCCAATACCAGCCCCAGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCTGAGCCTAGTACCCCAATT
182	106	C A ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCC[AC]TCTGAGCCTATCTCTCCTCCTATTT TACTTGAAGCTGCCAATACCAGCCCCAGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCTGAGCCTAGTACCCCAATT
191b	273	T A ---	---	ATAATTGCTGTTTCTAGCCTGGCAAGATATTTCTATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACACAGCACCATCTAAGCATTAGTATGGGTAGC TGATGTCAGCTTTCATGTGGATTTAAGCACTCTAGAACAAATGAAGCTTCTTGGCATATTTAAGGAG CTCCCAAATGTGTACCTATTAAATTTGTAACCTCAGCAAGTAGAGACCATT
199c	112	T C ---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT[AC]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCTTAATGTTTGTGTTTGGTCTCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA
199b	112	T C ---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT[AC]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCTTAATGTTTGTGTTTGGTCTCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA

WI-7216c	237 T C ---	---	---	TGACACTAAGACTCTAATTCAAGCGAATGTTGGAAACACCATGACCTCCTCTGTGTGCTCTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCTCCAGAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCCTCTGAGGCTAAACACAGTTTGTTCCTGTGTAATCAGTT
WI-7216b	237 T C ---	---	---	TGACACTAAGACTCTAATTCAAGCGAATGTTGGAAACACCATGACCTCCTCTGTGTGCTCTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCTCCAGAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCCTCTGAGGCTAAACACAGTTTGTTCCTGTGTAATCAGTT
WI-7220b	147 A T ---	---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTTATTTGTCTCTTTAAGCTGGCAAAACCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATATCTTGAGCACAGTGAATGACCTATCTCGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGACACATATTTAGTGTGTTT
WI-7220	140 A T ---	---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTTATTTGTCTCTTTAAGCTGGCAAAACCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGC[AT]CTAGAAAATCTTTGAGCACAGTGAATGACCTATCTCGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGACACATATTTAGTGTGTTT
WI-7226	232 C ---	---	---	GATCGAATTTTCAGATGATTCGGAAATTTTCATTCAGGATTTGTAAATAGTGACATATATATGATATA TACATACCTCCTATCTCTAAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGTATCATTT CCCTTTCCATATAGGAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAAAAATAA TTACCCACAATGCCACAGTAACCTAACGATCTTCACTTCTTGGGGTTT
WI-7228b	254 G A ---	---	---	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATGGCTCCCAATTCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTCTGCTTTGTAATCTATTTAGTTGATTTTAAATTA CTTCTGSAATAACGGAAGGGATCAGAAATATCTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTTAAATAAGAAATGTTATCCAACTATTAAGATATCTCAATGTT
WI-7228a	163 G A ---	---	---	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATGGCTCCCAATTCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTCTGCTTTGTAATCTATTTAGTTGATTTTAAATTA CTTCTGSAATAACGGAAGGGATCAGAA[GA]ATATCTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTTAAATAAGAAATGTTATCCAACTATTAAGATATCTCAA
WI-7233c	213 C T ---	---	---	CGATCGTACTGCCAGTAGCATTGCTGTGCTGCTCCGGCTTGTGTGATTCATTCATTTCAATTTTACA GATGTGAACCTTATTCCTTGTCACTAATTAATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTCTTCTGCCACCTTTTGTGCAATATTAAGTGAAGTGAAGTGA GTGTAAGTATCTGTGACACAAACCACTGCCAGATAACCCAGAGGGGCTG

WI-7233b	213	C T	---	CGATCGTACTGCGAGTAGCATGTGCTGTGTCGCGGTCTGTTGTACATTCATTTTCAATTGTTACA GATGTGAACCTTTATTCTTGCTCACTAAATATATTTAAATATTTCTAGGAAGTCAAAAAAATAAA TAAAGGGTTAGCCCTCTACTTCTTCTGCCACCTTTTGCGCAATATTAAAGTGAACGTGCTAATA GTGTAAGTATCTGTGCACAAAACCACTGCCAGATAACAGAGAGGGGCGCTG
WI-7233	211	T C	---	CGATGCTACTGCCAGTAGCATGTGCTGTGTCGCGGTCTGTTGTACATTCATTTTCAATTGTTACA GATGTGAACCTTTATTCTTGCTCACTAAATATATTTAAATATTTCTAGGAAGTCAAAAAAATAAA TAAAGGGTTAGCCCTCTACTTCTTCTGCCACCTTTTGCGCAATATTAAAGTGAACGTGCTAATA GTGTAAGTATCTGTGCACAAAMCCACTGCCAGATAACAGAGAGGGGCGCTG
WI-7238	128	T C	---	GCGTCTACAGACAGCTCACCAATTTTGCTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATGTATGTTCTTTAAATCGTTAATGTATAACAGGCTTATGTTTCAAGTTGTTTCTGCGGTT CTGTTTAAACAGAAATATAAGGAGTGTAGCTCTTTTCTCAATTTCAAGTTGCTACCAGTGTAT GCAGTATTAGAACAAAGAAACATTCAGTAGAACATTTTATTGCTCTA
WI-7252f	520	T C	---	CCACAGGATCCAGCCAGCGGCCCCCTCCGCCCCCTCCACTGCGACAGACGCCGGGACAGAG GCTGCCCCGGCGGCGAGCCCGCCCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGTTCCG GACACTCTAGAGAACGACGCCCTAGAGCCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252e	552	T C	---	CCACAGGATCCAGCCAGCGGCCCCCTCCGCCCCCTCCACTGCGACAGACGCCGGGACAGAG GCTGCCCCGGCGGCGAGCCCGCCCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGTTCCG GACACTCTAGAGAACGACGCCCTAGAGCCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252d	540	T C	---	CCACAGGATCCAGCCAGCGGCCCCCTCCGCCCCCTCCACTGCGACAGACGCCGGGACAGAG GCTGCCCCGGCGGCGAGCCCGCCCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGTTCCG GACACTCTAGAGAACGACGCCCTAGAGCCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252c	552	T C	---	CCACAGGATCCAGCCAGCGGCCCCCTCCGCCCCCTCCACTGCGACAGACGCCGGGACAGAG GCTGCCCCGGCGGCGAGCCCGCCCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGTTCCG GACACTCTAGAGAACGACGCCCTAGAGCCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252b	540	T C	---	CCACAGGATCCAGCCAGCGGCCCCCTCCGCCCCCTCCACTGCGACAGACGCCGGGACAGAG GCTGCCCCGGCGGCGAGCCCGCCCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGTTCCG GACACTCTAGAGAACGACGCCCTAGAGCCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA

WI-7252a	520	T C	---	---	CCACAGGATCCAGCCCAAGGGGCCCCCTCCGGCCCCCTCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCCGGCGGCGGAGCCCCGGGCGCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCGG GACACTCTAGAGAAACGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCCTCTCTGGAGGATGCAGGTGGAACCTAGCTAGCTAGCTCTCTCCCA
WI-7265m	252	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTAATTTTCTTTAAGGAGTAAGGATTTGCCTTT
WI-7265l	231	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTAATTTTCTTTAAGGAGTAAGGATTTGCCT
WI-7265k	121	T G	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTTCATTGTAGTT GTTTAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTAATTTTCTTTAAGGAGTAAGGATTTGCCT
WI-7265j	174	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTAATTTTCTTTAAGGAGTAAGGATTTGCCT
WI-7265i	227	T C	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTAATTTTCTTTAAGGAGTAAGGATTTGCCT
WI-7265h	80	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTTCATTGTAGTT GTTTAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTAATTTTCTTTAAGGAGTAAGGATTTGCCT
WI-7265g	170	T G	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTAATTTTCTTTAAGGAGTAAGGATTTGCCT





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WI-7301	205	A C ---	---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGGCGGGTATGGTGGTGGTGGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGGAGGATATGATGTTACAAATGAAGGAGGAAATTTTGA CGGTAGTAATACTATGGTGGTGGTGGAACTATAATGATTTTGGAAATACAGTGGACAAAGCAATCA AATTACJTGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7314c	49	G A ---	---	---	CTCTGCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCAGJATTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAACAAACTTGTTTTT
WI-7314b	49	G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCAGJATTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAACAAACTTGTTTTT
WI-7314	36	A G ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAJTTTGGGAGGTCAGTGTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAACAAACTTGTTTTT
WI-7321b	199	C T ---	---	---	ACTCAGGAAGGATGCCCCATTAAAGTGACAAAGGGTGGGTGGGCACTGGCATGAGGAAG AAACAAGTCCCTGAGCAGGACAAAGTCTGACAGTCAAGGGAGTCTTTGGCATCCAGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAAATCAAGNNNNNNNAGGTGGCACACCCATC[C /TGTGTTGCTGGGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199	C T ---	---	---	ACTCAGGAAGGATGCCCCATTAAAGTGACAAAGGGTGGGTGGGCACTGGCATGAGGAAG AAACAAGTCCCTGAGCAGGACAAAGTCTGACAGTCAAGGGAGTCTTTGGCATCCAGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAAATCAAGNNNNNNNAGGTGGCACACCCATC[C /TGTGTTGCTGGGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248	A C ---	---	---	AGACATTCGCTTCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAAGTGGCAGATGCTCAGGCTACTATAGGTCCAGAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAATAATCTGAATTTGGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAATTCATGATCAGATCTGGGGCAGCAACCTATAAATCAAC/CICA
WI-7338c	221	A G ---	---	---	CTCTTCTCAGCATTGATGGGCACTAGAAATACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAACAAACAGAAATCAATATATAAATCAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC/C/GTATACACACAGACATCAGAAATCTGTT

WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACATATACACACAGACATCAGAAAATTCGT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAGCTA GTGTTCTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATTCGT
WI-7338	221 A G ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATACCTTTAAATACCATTAATACATTTGATTTGATTTGTAACAGGATTTCTTCA CAGATCTCATT[T/A]AAATCTTAATGATTATTTTACTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAGAA
WI-7384c	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATACCTTTAAATACCATTAATACATTTGATTTGATTTGTAACAGGATTTCTTCA CAGATCTCATT[T/A]AAATCTTAATGATTATTTTACTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATACCTTTAAATACCATTAATACATTTGATTTGATTTGTAACAGGATTTCTTCA CAGATCTCATT[T/A]AAATCTTAATGATTATTTTACTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAGAA
WI-7384	145 T A ---	---	TGAAATCCTGGGTCTCTGGCTGTCTGTAGCTGGTTATTTTACTTTGCCCTCCACATTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACT[A/T]TAAAGGTTTTGAAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTTACCTCTATTTCGCACAAGCGTCTCGGATGTTTGA CTTGCTGTCCAAAGAACTTTCCCCCAAGATGTGTATGTTATGG
WI-7388c	106 A T ---	---	TGAAATCCTGGGTCTCTGGCTGTCTGTAGCTGGTTATTTTACTTTGCCCTCCACATTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACT[A/T]TAAAGGTTTTGAAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTTACCTCTATTTCGCACAAGCGTCTCGGATGTTTGA CTTGCTGTCCAAAGAACTTTCCCCCAAGATGTGTATGTTATGG
WI-7388b	106 A T ---	---	CTTGCTGTCCAAAGAACTTTCCCCCAAGATGTGTATGTTATGG

WI-7398	94 T A ---		TGAAATCTGGGCTCTGGCCCTGTCCTGTAGCTGGTTATTTTTTACTTTTGGCCCCCTGCCACTTTTTT TGAGATCCATCCTTTATCAAGAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGTTACCTCTATTTTGGCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAGAAGACTTTTCCCCAAGATGTGTATAGTTATGG
WI-7438	64 A G ---		TTAGATTTTAATTGGCAACCCAGCAACTCACTGCCACCATTCCACTGCAGATCTNCTATTCTCTGG(A/G) GTTGATATGACAAGGAACCCCTATTGGAACCAAGCTTTCAGATTGTCAGATTGTCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTCTGTTCTACTGTAACTAGTTGTGTCGTTGTTGTTGTTA TTGGAAATGAATATCGCTTCCACTGACITTTTACCA
WI-7454b	152 T C ---		CCATGATCCCCCTCTTGGCAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAAACCCCTGATAGCACTGCTGAATGGCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTC(T/C)GTGTTTAAAGTTATTTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGCTACTTCTCAATGTTTTGACA
WI-7454	152 T C ---		CCATGATCCCCCTCTTGGCAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAAACCCCTGATAGCACTGCTGAATGGCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTC(T/C)GTGTTTAAAGTTATTTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGCTACTTCTCAATGTTTTGACA
WI-7464c	177 G C ---		AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACATGCACATAAATCTATTATAATTTCTCTATGTA CAACAGAGCCACACAGCAAGAGGGTGGGCATMGCAAGTTGCCA(G/C)CCAGAAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGCAAGGTTCCACCAACAATTAT
WI-7464b	168 C A ---		AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACATGCACATAAATCTATTATAATTTCTCTAT GTACAACAGAGCCACAGCACAAGAGGGTGGGCATAGCAGTTGCCAGCCAGAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGCAAGGTTCCACCAACAATTAT
WI-7464a	103 C A ---		CAATTCTCAATCCAAOCTAGTCTGNTGCTTAACCATTCAGACAAAACCTCCACTTCGAAGGTTTTA AATGCAATAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGCTTCTTTGAATGCTTCAIT /GJTATAGTCCTCTTCATTAGCAATAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAAATCCCTTTGAAAAATATAAATTTGGAAATGAGTATGA
WI-7499b	134 T G ---		



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WI-7576b	168 A T ---			AATGATGATGATGATGATGACGACGACGATGCTGTGTAACAAGAAAAACATAAGAGAGC CTTGGTTTCAGTGTTAAAAATTTTGAAGGGCGGTACTAGTTCAGACACTTTTGGAGTTTGTG TCTGTTTGTAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCTTATTCTACATTTCACTAC TTTGTAAAGTGAGAGAGACAAGAGCAANNNNNNNNNAAAGAAAAATAAAC
WI-7577q	77 T C ---			AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCAAT/CJCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTTACCGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---			AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA TAAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTTACCGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---			AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTACAC[G/AJTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---			AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA TAAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTTACCGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---			AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTTACCGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---			AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTTACCGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---			AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCAATCAAAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTACACGAGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC



WI-7577b	117 A G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGATTTTC
WI-7577	107 G A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAG/GJAGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGATTTTC
WI-7619g	106 C G ---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTC/GJCTGTGTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTC/GJCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCCT CGCTTCTTCTTACACAGAAACAT/GJACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCCT CGCTTCTTCTTACACAGAAACATACACATACCG/GJAGAAACCTATTTC
WI-7619m	99 C T ---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	---	ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCT CTCTCGCTTTCTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619j	206 T G	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCT CGCT[G]TCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619i	106 C G	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCT CTCTCGCTTTCTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619h	150 T C	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC CAGGAAGATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT TCTCGCTTTCTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619g	228 A G	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC CAGGAAGATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT CGCTTTCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619f	237 G C	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC CAGGAAGATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT CGCTTTCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619e	99 C T	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC TGGCAGGAAGATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCT TCTCGCTTTCTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619d	189 T A	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGTCTAATTAC CAGGAAGATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT TCTCGCTTTCTTTACACAGAAACATACATACCCGAGAAACCTATTTC

WI-7619c	90	C G	---	---	ACAAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCGCTCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTTGGGCTCTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619b	206	T G	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTCTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619	189	T A	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTCTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7626d	105	A G	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGC[NG]TTAAACCAATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCGCTGTGATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626c	155	C T	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTGCCA TACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCGCTGTGATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626b	28	T A	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAG TAATCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCGCTGTGATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626	144	T C	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTGCCA TACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCGCTGTGATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7689c	134	A G	---	---	TCCCATACCGCTGATTCAGGGTCTCTGTGCTGCCGCCACCCAGATGGGGAAAGCAGGTTGGGC TCCCAGTGGCTGTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC

WI-7689b	134	A G	---	---	TCCCATAACCGCTGATCTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCTCTAAQA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGMATTCATATGAC
WI-7689	121	GA	---	---	TCCCATAACCGCTGATCTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCTCTAA AATAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGMATTCATATGAC
WI-7690	45	GA	---	---	TGGAGAACATTCAATCTTGCCGTCACATTCATCAATGAAGATTAGACATGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCACAGCATGTAGTGGCAAAGAGAGTCCAGAGTCCCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGATGAGGCCACCCAGGAAGCAC AGTCCAAAGGCTGGTCCACACTTATCAGCAGCAAACTGTCAGTTCAATCC
WI-7703b	164	T C	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTACATTGGAAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAATTAATTCAGTCTGCTGCTGTTTATTTAACTCTCTAAATCT TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156	T C	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTACATTGGAAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAATTAATTCAGTCTGCTGCTGTTTATTTAACTCTCTAAATCT TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	CA	---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTACTGCGGCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275	CT	---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTACTGCGGCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106	CA	---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTACTGCGGCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC

WI-7743d	275 C T	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275 C T	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275 C T	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275 C T	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G	---	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATTAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAAGATCTTCAGAGACTTCGTAATTAAGGAACAGAGTAGAGACATCATCAAGTG GAGAGAAATCAGTAGTTAACTGCAATTAATAATTTTAAAGAAATTAAGTAGATTTTAAAA GATAAATGAGTAAATTTGTTTATATTTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126 G C ---	---	ACAGGGCCTTTGGCAGGTGCAGGCCCACTGGCTTTGACCTGCCCTTCATGCGATGGAATTCCT TCATCTGMACCATCAGAAACACCTCACACTGGGACTTGCAAAAGGGTCAGTATGG[G/C]TAGG GAAACATTCATCCTTGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCTCATGCTGTG ACTAAACCAAATCACTGACCTTGTGAGCCTGTAAATAAAGGTCGGA
WI-7773b	237 C G ---	---	TTAATTAAGTATCCAGCAAGACCAATCATTTGATATCAGATTATTTTAAGTTTATCCGTAGTTTT GATAAAGATTTTCTATTCCTTGGTTCTGCAGAGAACCTAATAAGTGTACTTTGCCATTAAAGCA GACTAGGTTTATGCTTTTACCTTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTT GATTTTCGACGTTTGACTAGCCATCTCAAGCA[G/C]TTTCGACGTTTGA
WI-7774b	170 T C ---	---	TGCAACCTCTTTCTGATGGGAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGAGCCACCCAGAAT CAGATCCAGCTTCGGCATTTGATCAGACCAACAGTGTCTCCCGGGAGGAACACATTTTAA TTACCTTTTGAGGACCACTTTAATCTGTTT[C]ATACCTTGTCTTATTAAATGAGCGACTTAA ATGATTGAAATATGCTGTCTTTAGTAGCAAGTAAATGTGCTTGTCT
WI-7785c	165 G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCAATGGAATAAACTGTCTCCCCATTTGCTATGAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAAATTATTATCACATTTACCA TAAATTAATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTGTGC
WI-7785b	165 G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCAATGGAATAAACTGTCTCCCCATTTGCTATGAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAAATTATTATCACATTTACCA TAAATTAATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTGTGC
WI-7785	156 T ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCAATGGAATAAACTGTCTCCCCATTTGCTATGAACTGC ACATTGGTCATTGTGAATANN /TNNNNNNNGCCAAAGGCTAATCCAAATTATTATCACATTTACCATAATTTATTTGTCCATTGA TGTATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84 G A ---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCTCCCTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGTGACTCGGGGCTGTCTCAGACGACTAGCCCCAGGACCCATCT
WI-7789b	84 G A ---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCTCCCTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGTGACTCGGGGCTGTCTCAGACGACTAGCCCCAGGACCCATCT

WI-7789	73 GA ---	---	TCCTCCCTCATCCAACTCGAAAGTCTGAACTCCCAAGGAGGGCACCACCTCTTACAGAGACTCTCCG TGACG/GATGGAATTTAAGTTAGGGTCCCTAAAGCAATTTGACACACAGATTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTACTCGGGGGTGTCTCAGACCACTAGCCAGGACCCCATCT
WI-7790b	190 CT ---	---	AATTGTCAGTCACCTTCTCAAAACCTTACAGTCCCTTCTAAGGTTACTCTTCATGAGATTCACCAT TACTAATCTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTCTCTATTTCTTGAACCTC/GTTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190 CT ---	---	AATTGTCAGTCACCTTCTCAAAACCTTACAGTCCCTTCTAAGGTTACTCTTCATGAGATTCACCAT TACTAATCTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTCTCTATTTCTTGAACCTC/GTTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81 CA ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCCTTGGCTCATATTTCTTCTTCAT CTTGATGATGATC/GATCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTCTTCCAGAAAATTTCTCTTGAGGAAAATGTCCAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7795	81 CA ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCCTTGGCTCATATTTCTTCTTCAT CTTGATGATGATC/GATCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTCTTCCAGAAAATTTCTCTTGAGGAAAATGTCCAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7814c	41 GA ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG/GATTTTATTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTCTTTCTCTGGTAAATTTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG/GATTTTATTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTCTTTCTCTGGTAAATTTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGTTTATTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTCTTTCTCTGGTAAATTTGACTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150 C T ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCAATCATCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAAATGTACACATTCGATTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTTGA
WI-7830c	54 G A ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAGTCTGTCTGATGA TGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCAATCATCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTTGA
WI-7830b	134 G A ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCAATCATCTATGCCAAACAGGAAC G/AATCCATAACTTTAGTCTTAATGTACACATTCGATTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTTGA
WI-7830	44 A G ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAGTCTGTCTGATGA TGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCAATCATCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTTGA
WI-7865e	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGCGAGGCAATTCAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCCGAGTAAACCCAAA
WI-7865d	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGCGAGGCAATTCAGTCTCCACAAACATCTA ATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAATCTCAATGTTCTCAGTAC[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCCGAGTAAACCCAAA
WI-7865c	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGCGAGGCAATTCAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCCGAGTAAACCCAAA
WI-7865b	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGCGAGGCAATTCAGTCTCCACAAACATCTA ATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAATCTCAATGTTCTCAGTAC[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCCGAGTAAACCCAAA



WI-7865	25:CT ---	---	CCACTTCCTATCTGATTTTCCAG[C/TTAAATGAGGCGAGGAATTCAGTCTCCACAAAACATCTAGGCCATCTAAATGGAGAGATGATCAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTATAAGATTCAGGGTGCTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAACCTGAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCCAA
WI-7865	191:CT ---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGCAAGGCAATTCAGTCTCCACAAAACATCTAGGCCATCTAAATGGAGAGATGATCAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTATAAGATTCAGGGTGCTCCAACTGAAATCTCAATGTTCTCAGTACGTA[C/TTGAAAAACCTGAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCCAA
WI-7867c	92:AC ---	---	TTCAAACACCTGTCTCCACCCCTCCACCATCTGTGCAATCACTTCACCCCTCAGCCCTCACTAGTCCCTCTAACAAATTACCTGTCAAGAGG[C/GAGTGCAGCTCAGGTGGATTTAATGTGGGTTTAAATGGCCTGTTGAGTTTAAATGTTAATGTTGATTTCTTTAAGTAACCATTCGTCTTGGCTATATAATCTATGTTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92:AC ---	---	TTCAAACACCTGTCTCCACCCCTCCACCATCTGTGCAATCACTTCACCCCTCAGCCCTCACTAGTCCCTCTAACAAATTACCTGTCAAGAGG[C/GAGTGCAGCTCAGGTGGATTTAATGTGGGTTTAAATGGCCTGTTGAGTTTAAATGTTAATGTTGATTTCTTTAAGTAACCATTCGTCTTGGCTATATAATCTATGTTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173:CT ---	---	TTGATCGATCTTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAAAGAGGCTTAAACCCGGCTTTCACCCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAATCATTTAATTTCCCTGCTTACCCCTATTCAAGCA[C/TTAGAGGCCAGAAAAATGGGCAAAATTATCACTACAGGCTTTGACTCAGGTCCAGTAGTTCTATTCTAATGCCTAGAT
WI-7868b	173:CT ---	---	TTGATCGATCTTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAAAGAGGCTTAAACCCGGCTTTCACCCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAATCATTTAATTTCCCTGCTTACCCCTATTCAAGCA[C/TTAGAGGCCAGAAAAATGGGCAAAATTATCACTACAGGCTTTGACTCAGGTCCAGTAGTTCTATTCTAATGCCTAGAT
WI-7868	66:TC ---	---	TTGATCGATCTTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAAAGAGGCTTAAACCCGGCTTTCACTACAGGCTTTGACTCAGGTCCAGTAGTTCTATTCTAATGCCTAGAT
WI-7870b	85:TC ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGGGTGGGGTGGCGGGAATCC[C/ATTTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGAGCTGCAAAATTCCTGCAAAATGAAATCCAATCAGGACTAGAAATTTAAACATCATCTACTGCCATCTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG

WI-7870	76 C T	---	---	ATCTTGCTCCCTGCAAGAAATCAGCCATAAAGAACGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGTGGC/TGGGAATCCTATTATCAGACTCTGTAAATGAATATAATGTTTTACTCAGAGGAG CTGCAATTCCTGCAAAAATGAATCCAATGAGCAGTAGAATATTTAAACATCATTAATGCCCCATC TTTATCATGAGCAGACATCAATTACAAGCTGTAGACCACCTAATATCAATTG
WI-7889c	54 C	---	---	TTAGGTCTCATGCCACTCCCGCAGGAGCAGCTGGCAGCTGACAGCCCTGGGGGGGGCGCTCTCCCGCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCCGGGGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCCAAGGCTGTCTCTCCAGAGCACAAGAAG
WI-7889b	54 C	---	---	TTAGGTCTCATGCCACTCCCGCAGGAGCAGCTGGCAGCTGACAGCCCTGGGGGGGGCGCTCTCCCGCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCCGGGGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCCAAGGCTGTCTCTCCAGAGCACAAGAAG
WI-7894c	142 A G	---	---	AGCCAGCCCCAAATATACTGTTATCCAGAAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTGTGAATTTATATTTGCGTATAC ATTATC/AGJTATGTAATAATTTGCAATTTTTTTATTGAAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G	---	---	AGCCAGCCCCAAATATACTGTTATCCAGAAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTGTGAATTTATATTTGCGTATAC ATTATC/AGJTATGTAATAATTTGCAATTTTTTTATTGAAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJCTGCCATTGAAACAGTGATTAAAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCAGTGAAA TATGATGTTATTTCTGAGCTAAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJCTGCCATTGAAACAGTGATTAAAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCAGTGAAA TATGATGTTATTTCTGAGCTAAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJCTGCCATTGAAACAGTGATTAAAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCAGTGAAA TATGATGTTATTTCTGAGCTAAAACTCAACTATAGAAGACATTTAAAGAAATC







WI-8021b	57	C T ---	---	ACAACTCAGAAGGACTGTGCAAGTCAATGAGTCGCTGTGAATTCATCTGGAAC/C/CTGATCCC ACGCTTAGAACCTTCACCAAGGAGTTTCTTTGAGTGATCTCAAAGTCTGGTAGGCATTGGA ACTGGTCTTACCTTGAGATCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTTAGGGGTGATTCGAAITCGGTGAATTGCCA
WI-8021	57	C T ---	---	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTGTGAATTCATCTGGAAC/C/CTGATCCC ACGCTTAGAACCTTCACCAAGGAGTTTCTTTGAGTGATCTCAAAGTCTGGTAGGCATTGGA ACTGGTCTTACCTTGAGATCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTTAGGGGTGATTCGAAITCGGTGAATTGCCA
WI-8024c	206	A G ---	---	CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACCTCCCATGGGAAGACAGAAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCATCACCACAACACCATTTAGCCGCTCTAGCCTCTAA TTCCG/C/CTCTAGAACAGCTGGCCCTGGTCTGCTCAGTACACAAAGGAAGAGC
WI-8024b	206	A G ---	---	CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACCTCCCATGGGAAGACAGAAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCATCACCACAACACCATTTAGCCGCTCTAGCCTCTAA TTCCG/C/CTCTAGAACAGCTGGCCCTGGTCTGCTCAGTACACAAAGGAAGAGC
WI-8077	167	A G ---	---	GAATGAGCCTCTCTAGCGCCGAGGAGCTGCTGCTGTTGTGGCTGCACATGCAATCTATGGAATGC TTTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAACCTCTTCT AAGGAGCTCGGGGTGTCATGCCCTACAAACQ/AG/JTAAATCTCATCAGATGGATTTATTTAACGTT GTGTAITGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114	GC ---	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATTTTGG/AVJTGACCACCTCCCTTGTAAAGGAGC GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGTG/C/JTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G ---	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATTTTGG/AVJTGACCACCTCCCTTGTAAAGGAGC GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G ---	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATTTTGG/AVJTGACCACCTCCCTTGTAAAGGAGC GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGA/C/TCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTTGTTTCTTAGCCTTGAAAGA TGACCAGGTAGAGAGACAGAGTGAGACCACAGATTTTCTGATTTCCCTGCTCCTCTATTCCTCT AAAATCAGACTCATTTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAC/T/CJGGCAATACAGAATGTAGCTTGTTGTTTCTTAGCCTTGAAAGA TGACCAGGTAGAGAGACAGAGTGAGACCACAGATTTTCTGATTTCCCTGCTCCTCTATTCCTCTCT AAAATCAGACTCATTTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTCTGGGGCATACAATGGCAGGCGCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCACACA TTTATGGAGGGTTGCCCTGAAGAAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAAAGACACAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTCTGGGGCATACAATGAJTGCGCAGCAGGCGCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGGTTGCCCTGAAGAAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAAAGACACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTCTGGGGCATACAATGAJTGCGCAGCAGGCGCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGGTTGCCCTGAAGAAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAAAGACACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTCTGGGGCATACAATGGCAGGCGCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCACACA TTTATGGAGGGTTGCCCTGAAGAAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAAAGACACAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---	---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTCTAAGGGG/C/JAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGTCTGTAGTCTTATGATGATCTAGAAGGACACTGTCCAATAGAATTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCATAGGGGTAACTACT
WI-8314	78 C G ---	---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTCTAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGTCTGTAGTCTTATGATGATCTAGAAGGACACTGTCCAATAGAATTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCATAGGGGTAACTACT

WI-8321	178	G A	---	---	TTTTAAATATGCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAAATGTTGTCAG TGATATACCCAGGNAATCCATTTCTGGTACTTTTCAAGAGCTGCTGTTATCTAGTACTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A	---	---	TTTTAAATATGCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAAATGTTGTCAG TGATATACCCAGGNAATCCATTTCTGGTACTTTTCAAGAGCTGCTGTTATCTAGTACTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-832b	123	A C	---	---	TATGTACTACTTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTTTCCCTTCCCTGTGCA/CJGCTTAGAACTAAGTAG CAGTACTGTTGGTGTGTTGTTCTTCCCGAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C	---	---	TATGTACTACTTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTTTCCCTTCCCTGTGCA/CJGCTTAGAACTAAGTAG CAGTACTGTTGGTGTGTTGTTCTTCCCGAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATATCATGGCAGAGGGCGAAGG GGAAGCAAGGACCTTCTCACATGGCAGCAGGAGAAAGAGAGAGAGGGAAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATAGA AACTGCCCCCATGATCCCAATCACCTNTCACCAAGGCCCTCTCCAAACACGTGGGG
WI-8378	308	T C	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATATCATGGCAGAGGGCGAAGG GGAAGCAAGGACCTTCTCACATGGCAGCAGGAGAAAGAGAGAGAGGGAAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATAGA AACTGCCCCCATGATCCCAATCACCTNTCACCAAGGCCCTCTCCAAACACGTGGGG
WI-8426	184	T G	---	---	TTTAGCACATATTTAGCATTAAAGCCTCAACGATACAGCAATATGTTACATCTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNAAATGTAACCTCGACTTGGCCTAATAGGATTTGACCNNTAA GAGNTTCTTTTCTGTGGANGGGGTGCTTGTGTAACCTCCATCTCTGTG/GCCTTGTAGCTGGTG AGGCTGGAGATGGANGGNCCTGGGGGGCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C A	---	---	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTCTCTACATACACTC/AJCA TCCTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATATACCAATTTCCATTGTTATTTTAAAGA AAAAACCTCCCAGTTATGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT



WI-8450g	55	T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/CJACACTCCAT CTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108	T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125	T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125	T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108	T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATTC/JACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61	C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT TCTTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55	T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/CJACACTCCAT CTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60	A G ---			CAAGGAAAGCTGTGAGTCTTCATTAACCTTCAAGAGTTTCAAAAAATACGTTATTTTAAAG/CJCTA CAATTCAGATTAGCATCCAAACCTACAACATGATGATACATTCGTACACACCATACAACCTTCAC ACCTGGGTACAGCAATGTTGACTTACATCACCATTGTTTATACCTTGTAACAACTTTTATGTCACAGT GACATCCATCCGCCAGACTTAAATGTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACCTTGAAGACAATAAATACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATACTTGAAGACAAT[C/G]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATAATCATTTTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATACTTGAAGACAATAATACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACTTGAAGACAATAATACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGGTAGTACTTAATTTTGATAAAAAAAT TAAAAAGCAT[G/A]ACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAAATATCTCCCTTTGTTTGTCTTTTAAAAACATTATTTCTGAAAAA ATCAGAAAAACATGATCGTGGAGAAATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAATTGACCTTTATTTGTTGTAATAAGCCCTGTTTAACTTTGATACAAAAGTAACATTTTAGTA CAGAAAATCCCAGTCTGCAGCTCAGTACCTG[C/T]GTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACCTAGAAAACAGCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9439a	76 C T ---	---	---	ACAGAAATTGACCTTTATTTGTTGTAATAAGCCCTGTTTAACTTTGATACAAAAGTAACATTTTAGTA CAGAAAAT[C/T]CCAGTCTGCAGCTCAGTACCTGCTGTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACCTAGAAAACAGCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9446b	75 T C ---	---	---	GAAAGCTTGATTAAGGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAGANCATT TAAAAAAA[A/T/C]CCTCTAAAGNGACACATGCCCCAAATGACANGNCATAAGCAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGNNCCCTACTNTTATCACTGTGCTCTTCTGCTTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

WI-9446	75	T C ---	---	GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGNAACCTTACCATTCCATAGACTATAAAGANCATTAT TAAAAAAATG/C]CCTCTAAAGNGACACATGCCCAAATGACGANGNCATAGCAAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGNCCTTACTNTATCACTGTGCTCTCTGCTCTTTTGCTACCTA TGNGACTCACACTATCTGTGGCAATATTGT
WI-9497b	185	A ---	---	ATTAAAAATGTCAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACATCTTTT GAGATAATTAATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGCTCTCCAAATTTNCITTAATTAATCAAAAGTATGTTAATGTCACIT GGAATTCATACATGGAAGGCCAACAAATAACTAAACTTGACTAATGAAG
WI-9497	185	A ---	---	ATTAAAAATGTCAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACATCTTTT GAGATAATTAATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGCTCTCCAAATTTNCITTAATTAATCAAAAGTATGTTAATGTCACIT GGAATTCATACATGGAAGGCCAACAAATAACTAAACTTGACTAATGAAG
WI-9523b	193	C A ---	---	GTGAAAAAGTTTCTATTCTCATCATACATAGATTGTGCTAAGGATCATTTTGGAGAATGTG CAGCATTCAGAAAGTTGATCTCATCATGCGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGTTGATTTCCACACATTTGTA/C]AAGTG AAAGCTTTCAGCTTGAACAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G A ---	---	GTGAAAAAGTTTCTATTCTCATCATACATAGATTGTGCTAAGGATCATTTTGGAGAATGTG GTGCAGCATTCAGAAAGTTGATCTCATCATGCGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGTTGATTTCCACACATTTGTACAGTGA AAGCTTCTCAGCTTGAACAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9554	202	T C ---	---	AAAAACAAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAGTGATTATTACCAGAC AAGCATCAGTGATGATACCTGCTTCTAGTTTGTATGTAATGCTGTAGATAATGCAGCCCATG CAATACACCCAAAGAACTAGAGTCTACACCCCAAGTACAAATATGATAAGCAGCCCTCTGCAAGTG GT/C]GCTGGATACCACTAAGAAAGTCTACTGAGCCATGTTGGTTATGATTTT
WI-9555	97	G A ---	---	CCAAAAGCCAAACCATTCATATGATGGATTTCATAAACATTTTATGATCCTTTTGGAGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC[G]A]CTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAAAATACAGGTAAATTCAG GGNTAAATGGTACAAAAAAGGCTGTAACCTTTTNCITTCACATTGATCACA
WI-9625b	172	A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACATAGCTACCATATATTTGATCTNCTCTTGGGAAAAAACCTTTGGAAAAAACAACGCACA TAAGTATCATAACTGAGGGTGTGGACAAAGTTACTTCTA]T]GTTTACCAATTTTATATGACATAA AGTAGCAGACACTAGTTATTTTCATTTAAAAAAAACACACTGCACAAATCTTTTC

WI-9625	172 A T ---	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGGAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAAATTTGGAAAAAAACACGCACA TAAGTATCATAAAGTGGGTTGTGGACAAGTTACTTCT[AT]GTTTACCAATTTTATATTGACATAA AGTGCACAGACTAGTTATTTTCAATTTAAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	---	TTTTCTGAGATTCAAGAGCTACATTTTGGTAGTGATGCTACTATACCTTTTTCCTCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTTTGTAAACAGTGTATTGTAGACCTAAAAATCCAAGCT TACAACT[CT]GTCTTTACCTGATACATTTATCCATTACTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGTCCTGCTTTTAGTTAAITGTGTTT
WI-9676n	114 A G ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676m	184 G T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGG[GT]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676l	84 A C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676k	202 C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA C[CT]CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676j	92 C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676i	173 T C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ C/AJATTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGAGG C/T/CAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGC/T/CATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTT/CJCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCA/A/GJGATGTGGCTTTCTGCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCA/A/GJGATGTGGCTTTCTGCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT

WI-9738b	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACATCATTTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATAAGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACTTGCCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCITTTATTCTGTCCCTTAITGTTGGTGGCACAIGICTGTAITGCTGTC
WI-9738	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACATCATTTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATAAGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACTTGCCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCITTTATTCTGTCCCTTAITGTTGGTGGCACAIGICTGTAITGCTGTC
WI-9756	47	A ---	---	ACTGAATGTAAATGGCCAAGGCCACCCAGGACCTTAAATCATAGAAGTTAATCTGTGGGAAAA GAGTAACACTACAAAAGCATCTAACAAAGAGCAGGATGTGATGTAATGTGCCCTTATCAGCTTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAACACACAGATAATACACTTTTGGGAG ATTCCACTTAACCACTTGATCTTCACITTTTATGATTTTAAACTCTCCGTGG
WI-9758	135	A G ---	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATGAATAAT TAGGAAACTGGGAGAAATCAATTCAAAGAAGAAATCTTGTTCGAAGGTCAATTTTATACTATTTA A[A/G]TAAATAAATCTCTGGTAGGTTCTATAGCAATGCTAAGTAAAGTAACCGCTGGTTCTAAAT ATTACG
WI-9778	127	G A ---	---	ATTTAAATCCAGGCGGGGAAAAATGGATACTTTCATATGCTCTGTACCCCACTATAAACTTTTG GTTCTCATGGACCAATTTTCAATTTTGGCTTCTCAGTCCAGTACCAGTATTTTACCAATTT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCCTCA AAG-AATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---	---	TCTCCCTTTGCCCTCTCATGCCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAAATGCAGTTT[C/A]TGGATCCCACCCAGGA CTCAAAAACTAGGAATGGGAGAAAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101	A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCCTATTTTGAATGAATAAAATATAC[A/G]TGTGTATGTATATATATCTTAAACACTT AGGATTATATACACACAATAAAACGCTGTAAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTTACTTGATATGCTGTTG
WI-9880c	222	G A ---	---	GAACATAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAAACAATAAATGTTATTAGATC ACTGGTGCCTCTGTGTGGGTTGAGTTTTTATGATATCTCCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATTAATTTTATATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATACCTACATATTTTG

WI-9880b	157 C A ---	---	---	GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGA[C]ATATAAGATCCTCTTTTAAATATATTTTATATAAGCACAT GAAATGGAATGAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108 C T ---	---	---	GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATATAAGCACAT GAAATGGAATGAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127 C T ---	---	---	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAAAACAACGCCAGTTATCACAGTTTCTNTTTTGT[C]T[CACC ATTTCCATAACAAAAGAAAGCTACACAAAATNNGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109 A G ---	---	---	TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAGAAATACITTTATGTCCTTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA[A]GJTGATTTTAGATCCTCCCCCAG TGACAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109 A G ---	---	---	TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAGAAATACITTTATGTCCTTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA[A]GJTGATTTTAGATCCTCCCCCAG TGACAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102 C A ---	---	---	ACAAAGCTGAACCTTCCATAACAGTCAATGGTACAGTCAAAACATCAGATGTACAGAACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAAT[C]A[C]AATTTTCAGNAAACAAAATCAAAC ATTAAGGNTCCCTGNNATATCTTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCCTATTAAACCCAGTCTAGGGATTCTG
NIB551	161 C T ---	---	---	CGTCTTTCTCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAACTGACAATGGGTGTGCCC TACTGAGCTTGGGCCAGGTGTGACTTAGGAACCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C]T[T]GACCACATACATCGGCCATTGGTTGATTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTC
S72904	51 G T ---	---	---	AGCATAGAAAGTGATTTATATTTTAAATGGTTTCAAGTGGAAAGTTCTT[G]TAAATTTGTCAGTTT ATTCCTGGAAATCTTTGAGTTAAATAAGCATCTAGGACGACACCTCAGAACTACAGGCCCTAAA GAGAAATTCCTCAACCAACAAGTGCTGTAACCTCTCCCTTCTGTCATTTGGTTGCTCTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTCTTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TAATCTTTTATCTCTGGGCGCACAGTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC CATTAGATAAATGGCAGTACTTTAGGACACACACAAACACAGACATJACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGGCTCTGTTTGGACAAAAATAACNAGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGCTCCTCTCACANGCTGTATTACCTTTCAGAGCTGAGTGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTTCCTTTAATGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAATAAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANAATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGCGAACTGG
ESTC129	20	---	---	---	AGTCACCATGCCACGCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG



ESTC132	30	---	---	---	GGTAAAGTCTAAATTAAGTGCCTTAGCAACNCTATGTTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTGGCTTCTGCTCCANAGTCTCTCCATGTGGCAACA
ESTC139	45	---	---	---	AGGAGCAGCGCTAAGGACATGAAGTCAGAGTTTCTCAGAGGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTTGGTGCACAGGAAGNAGAGGAGGCCAGGTTCTTACTAGTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATACTATTTTATTCATTTTAAATC AAAGANACCATTCATTCCCTAACAAACA
ESTC143	29	---	---	---	GTTACGAAAGTACTGAAATGCTATTANTAGCTGAATTTGIGATTTCCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGNGCTTTTAGCAGCATTCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACAGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTTGCTACACAGACACTTAAGTACTGTATGCTGTGATGAGCGGCTGTGGAGGCCCTG GGGTGGCTGGGCTGTGCTGAG
ESTC149	28	---	---	---	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCIGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCCCATTTTTTCTTTTAAATACAAATCTACTGGTGCTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACCTCAATCTCTACATACATACAGTNTTGCAGGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCAATTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGCGGCAAAACAAANCTGGTGCTCGGATGGAGCGGGGGCCCTCA CCACCCTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTGAGGCACATCAGNACGTTGGTCAMTTTAGGCACGGTCTGGTTCTGCA GCTTGAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCACAAGGACAGGTT
ESTC160	38	---	---	---	TTTAGCATTGCTGGTGCACTGGGGGCTGAGCTGGGNGCAGTGGCAGTGTCACCTGGGCGCGTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	CTCTCGTCGGTTGCAAGTGGCTGTTGTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	TCATTCTCCATAGAATAATTGGTTTTGTAACANGAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGTCTGGATTAGAGGAAAGTGCCCGCTGTCTTCCATGACTT
ESTC176	23	---	---	---	CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	TGGTGGCTCTTTAAATACCTTCATTATATTTTCAAATTTTNCITTTATTTCTATTAAATACCTTTTAT TCCTTTTATCCCATAAAAGGCCAACCA
ESTC18	29	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCTGCAGGGCGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	GCTTGACTAGCGAGGTACATCACAATTTATAAAGTGCCAGATNAGTGTAAATTGTTCATCAGCTTG ATTTTACCTCA
ESTC187	24	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	---	---	TCATTAAACAGGGTTATGTCACACCCNTGTCAACCTCAAAACAGATGATACTCATCACTTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	AMAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	TCCTCAATACCACCTTCCCTAACCTTATCAGICTAGTAGTAAAGCNITTTCAAAGGAGGAAAAATGGGTTAC CTTCAGGGG
ESTC197	26	---	---	---	ATCTCCAGTGTCTGCTGCCTCCTCCNCGCAAAGTCTCCACAAAGCACA
ESTC20	33	---	---	---	AAGATTAGGACAGACCGGTATAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGGCTGTGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	TTTGGTGAATAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	TCTACTTGGGTAGTTTAGCAACATTTTAAANCCACATCCACAGATTGGTT
ESTC202	22	---	---	---	CTGCTGGAGGAGGACAGACGNCAGCGCGCTGGGTGGCGGCCAGAAAGGCTGGCGTGATGTT
ESTC203	27	---	---	---	CGAGATGAGCC
ESTC208	43	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAATTTACTGCAACTTTTGTAGAAATTTATTGTGTACT
ESTC210	29	---	---	---	AAGACAGTTGCA
ESTC212	27	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTAAAGG
ESTC214	21	---	---	---	CTAAGAGTGA
ESTC216	49	---	---	---	GATGAAGTGGCTTCTTTGGCGAAAGGATNAAGATGAGTGACGGTGACCTGTG
ESTC217	28	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGT
ESTC219	32	---	---	---	TCAAGTC
ESTC22	41	---	---	---	CTCCAGAGTCCTCTCTCANACAGGGGCAGGAGGAGTTAGGGAAT
ESTC223	27	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTTAATCACAGGTATNTTAGATTGGTCAGAAAA
ESTC224	37	---	---	---	CAAAAGACCA
ESTC225	20	---	---	---	TTTTGTCAGTAATGAGCAATACACTGANTGGAATCTGCATGATTAAATAACATAACAAGTTTAT
ESTC23	27	---	---	---	AAACACCCCCA
ESTC230	43	---	---	---	GTACACATCCTGGGGTGAGCACACAGCAAAANGGGTGGACGTCGACAGAGGTATAGGGTAAAG
ESTC231	24	---	---	---	GCAAAGGAAGC
					TCATTGAAGAAATTAAGGGTTTATTCTTATTCTTAATTGNGAGAATGCTTAATGTCACAGGCTACA
					TAAGGGCC
					CITCTGAAGCCCAAGAGAGGGGCAGAANGTAGTTCITTGATTTAAAAAACAGAAAGGGGAGGAGGA
					CGAAGGTAGATTCCCTCACATATTACAAAATACANAAACACACACACACACACACA
					TGCACGTACTCCCGACACGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAAGGA
					ATGTGTAGGATCG
					TTCTACTTTATTTTCATATTCACCACACNATAACGACTCCTTTAATTTAACTAAAAACCACACAGGGT
					TCCTGAAGGG
					GCTTCTCCACGAATTTGAAGACATATTGGCTGACCTGATACNTAAGGAGCGGCCAGAAATTAAGA
					CAAAAGGGTAGTCATATTCCCCANCAACAGCATGATAAAATAATTCAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNITTTCTTCCTCTATCCTATAAAAAAGGAAGCAGAAATCTC
ESTC3	20	---	---	---	CC CAGACATGACCTACCGTCCCGGCCCTCAATTCATATTTTATCTTGAGCGCGCTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATAATNTCAGTCGGTGATCATGTGAATATACAATAACAAAG CAATTTCTCAGA
ESTC33	25	---	---	---	AGCACTTCCAGCTCCTTGAGGTTGNGGACCGAGGAACTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTTNGGTCACAGAACICAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAATCATTTATGCTGATGGAAAGAAACCAT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTCCCCCTTCAC
ESTC45	37	---	---	---	TTTGAGGTTTGTGTGGAGTTTGTCTTTGTAACNCICTCATCATCGAGGCTATATATTA CTGTCCGTGGTGAGCCCTGCCGTGTCCCATGGCCAGGAGCCACTGGTGGGANNCCGGCAGATG TTTACCCTGT
ESTC50	56	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGGAGGTCAGGAGGAGNAGTGGAGGAAAGGACACCA AGT
ESTC56	45	---	---	---	AAGTGGGCCCTCCCAGTCCCTCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC57	20	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATNGTCCAGACTTCAGGAAAATGATTTCC ACATGGTAAGGCC
ESTC59	38	---	---	---	CTGCAGCACTTCACCTACCAATGAGCNITTAGCTACTTTTTCAGAAATTGAAGAGAAATGCATTATG TGGACTGAACCG
ESTC6	27	---	---	---	AGTGATTTGGCTAGCGGTGTTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC61	57	---	---	---	ACAGACACAGCATCACACANAGGGCCACGGAGGGTCTGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC63	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC69	20	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCCTGAGTTGCANGCAGATGGAGATTTGGACACT G
ESTC7	45	---	---	---	

ESTC72	37	---	---	---	GGGCTTCCAAATGGGTATTGGGGCCAGGAGGCTGGCNITTTGGCGTGACGCTAAAAAGTGTGACC AACAAATTCACAGCTACAGGAAATCTAGAACAAATCAAAATATTCATCACNTTGGGTGAAAAGTTG GAAGA
ESTC74	49	---	---	---	ATGACTTCCCTGTCCCATCGGAAACCAGAGTTTCCCCAGNGAGCCCTTCTATCTGCGGTTA
ESTC77	40	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCGCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGGTCTGAGATGNTCCTCAGGCTGCATCAGCTGTCTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC81	20	---	---	---	CAAAATCAAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGCTATACCAAGTTCCATAAANCTGTCTGTGTTGGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC83	53	---	---	---	ATTGCAAGGAAGTGAACGTGNTCAACAGAAATGGTGACAATGA
ESTC85	28	---	---	---	CTGGTCTCTCGTCTGGCAITCGTCTCCTCCTCNGGCCAGTGTCCACCAAGTGTCTTCCCGATGAT
ESTC89	22	---	---	---	CTCCCTCCTCAGTTCACAGTGAGACTANGGAGATTAGGGCAGGATCC
ESTC90	33	---	---	---	GCACGTTCTTTGTTCTCCTCTCCAGAAAGTTGNAGACGTCTATTAGTTTGAATTATCTGTCG
ESTC93	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTTAATCA GTGGATCTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGAAGTGTCTCCAC/CTGGCAG ATTCTTATCAATGATCTTTACCTAAGAACAGCAAGATTCTGGCAAGCAGCATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAATCAAAAGAAAGAAAGGCTTAGCTG
DWU-100	127	CT	---	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTTCAAACAGAAAGACGCTTGTGCTGAA TGTTCAATGGC/AGJGCCCCTATTACAGTAGCCCAACGATGAAAACACCCCAAGCTATATATACCA GATGAAAGGATAACAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-177	77	AG	---	---	CAAAATACCTGGACTATCAACCTTGTGTCTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCCCAATCATGCCAGCTTGTGTCATGAATGAGATATACATTT ATGCTGACCTCCCTCAAGACTGATTTTTCATGCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG/ACTGGGAAACCAGCCCTATCTGAGTCTTCGGCTCCCTCC
DWU-286	213	AT	---	---	

DWU-252	94	A G	---			AGTATACAAACATTTAAGCTGGTCAAGGCTACAGATGTGCTGACAAGGCACCTTCATGTAAAGTGT CAGAAAGGAGCTACAAAACCTACCTCAAGTGTGAGATGGTACTTGGCCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCTGTTGAATGACAAAGTATGTGGTTTGTGTA AT
DWU-330	85	C T	---			GAACATTCCTCTGAGCAGCCTTCACTACCAAAATGAGCATTAGCTACTTTTCAGAAATTTGAAGGAGAAAA TGCATTATGTGGACTGAAC/TCGACITTTCTAAAGCTCTGAACAAAAGCTTTCTTTCCTTTTGC CAAGACAAGCAAGCCACATTTTGCATTAGACAGATGACGGCTGCTCGAAGAACAAATGTTCAGAAAA CTCGATGAATGTGTTGATTTGAGAAATTTTACTGACAGAAAIGCAATCTCCCT
DWU-370	231	A G	---			GAAATGTTAATTGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAGAG AAGCATCATTTCCCAACACAGGGCACTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGAAAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAGAAAAGTCT ATTAGACGGTACCAATTCAGTGTCTGTTCTTGA/GGCATCTATTTCCTCTGTGC
DWU-1537b	89	A G	---			CTCTTAACITTCAGTTCCTCATCTATAAGAATAAGGGATTGAGTTGTGATCACATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGC/AGTGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTCTGTAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C T	---			CTCTTAACITTCAGTTCCTCATCTATAAGAATAAGGGATTGAGTTGTGATCA/C/ATAGCTCAGGTA ATCCAGGACCAAGAACCCAGGAGCAGTGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTCTGTAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C G	---			ACCATCTTACTATGCGAGGTAAGTCCATACAGAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATTCAGGGTCACTGTCTCTCCCTGCTCCCTGTTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGGCCCTG/AG/CACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGTCTTGTCTC
ESTD-ADAA	184	G A	---			ACCATCTTACTATGCGAGGTAAGTCCATACAGAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATTCAGGGTCACTGTCTCTCCCTGCTCCCTGTTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGGCCCTG/AG/CACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGTCTTGTCTC
ESTD-ANT1	160	T C	---			TCTCTGTCTACTCTACTCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAAACAAATAATTCA TGGACTGCCCAACTGCGAAACAAGAGGGCGCAGTGGAGCAGGATATTATGCTACGCGGTACCTT TTTTATGGAGACCGCAACTGAGGCT/C/GAGCTCAGATGATCTCTGT
EST10398 2b	168	A G	---			TGCCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTTGTTTCTTCGGGCCAAGAGGTATCTACC/AG/ATAGTGTCTATTAGGCATTTG

EST10398 2a	147 C T ...			TGCTGGGTGGGAAGGCTGCAAAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTTGTTCTTCTTGGGCAAGAGGATATCTACCAATAGTGTCTATTAGGCATTTTG
ESTD-C7	14 G C ...			ATAICGTGGCCTTAGCTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ...			CTTTATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACATTTCAAGG ATAATGGGGCAATCACCTTTCTTTTCTTTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ...			AGTCTTCATCTGCGGTGCCAGGTAGATCCCTTTTACCCG/AJCCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ...			CTGGGCTGCCCCGACAGCTGCTGGCACCTGGACGGCGGCCAGGCTCACCTCTATAGTGGGGTCG TATTCGTCCACAAAG/GTTCATCTGGATCAGCT
ESTD- HRASa	37 C T ...			CTGGGCTGCCCCGACAGCTGCTGGCACCTGGACGGG/CJTGGCGCCAGGCTCACCTCTATAGTGGGG TCGTATTCTGTCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ...			GGAGGCAGGAGGTGGGGAGGGGCTGCTGCTGCTCCAGGTCCACAGACCAGAGAGCGGCCTCAGTG TATCCCCACCCCCA/GJTGTTGGGGCTGGGAGATGAAGAGGATTTGATGCAGGT
ESTD-OTC	18 A G ...			GTGACCTTCTCAGTTAA/GJAAACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAACAGAAAGGAGGATGTAAACA
EST36751 7	36 C T ...			CCAAGTCGTTCAATTTAGCTTTCAGGTTTAACTCTTGATTACTTTTCTATTCAAATCTCTGTA AAATTGAATATGAACTTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	109 A G ...			CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAGAATCTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAATTTTCACTGGATGCATTAATAACAAAT/GJTTTACCCTTTGAAAAAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAGAGATCCGTACCGTCTGACGTTTTTGAACAATACA GATGCCCTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	121 C T ...			GCCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTAGAA GATTGACAGGTTTCAAGCAGGCTGTACAGGATGGAAGACTGGCTGCTCCCTGA/CJGGGAGCCAGT GTGGACAGCACCCCTGGCTTTCACACCTACGTCCACTTCCAGGTAAGGCAAAACCTCTCTGCTGGCTC TGCCCTAGGACTAGTATCC
ESTD-AK- 168	31 C T ...			GGGAGTGACAGCTAGAGCACCAAGGGGGCTC/TJTAGAGCTGTGTTCTCATGGAGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180 A/G ...			AATCCCAGCAGCTTTAGGAGGCTGAGGAGGATATCACAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAAACATGGTGAACCCCATCTCTACTATAAAATACAAAATTAGCCAGGATGGTGGTGCCTGT AATCCCAGGAGGCTGAGGAGGAGATCGCTTGAACCTGGGAGGGG/GJAGGTTGTGGTGAGCCGA GATGGACCATTTGCACCTCCAGCTGGGCAACAAGAGTAAACTCTGTCTC

EST70523 3	182 G T ...	...	TTCCGCCAGCCCCCATCTTGGACCCCTGTGCCCCCTCAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCGGTAACATCCGGCGGGCGCGCTCTGAGCACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGCTTGGCAGGGGCCAGCCCTGTCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
ESTD- APOA2	101 C T ...	...	CCAGTGTGTGGACGTCCTGTATCCAGCTACTCGGGAGACTGAGGCATGAGATCTTTTGAAAC CGGGAGGGGAGGTTGCAGTGAGCTGACATGCTGACACTGCACCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ...	...	CAGTGTATCTGGAAGCCTACAGGACACCAATAACCTTAATCATCAATGGTTACAGGAGGCTTT AAGTTCAGCATCTTGGCTCAGATGAAGGCCAAATCCGAGAGAGCCTCTAGAAAGATACACGAGAC CGAATGTATCAAAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGTAGGCCAGGTTTATA GCACACTGTCACTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	137 C ...	...	AGACCATGAAGGAGTTGAAGCCTACAAATCGAACTGGAGGAACAACTGACCCCGGTGGCGGAGG AGACGCGGACGGCTGTCAAGGAGCTGACAGGCGGCGAGGCCCGCTGGCGCGGAGATGGAGGA CGTCCGCGCGCTGTGCAGTACCGCGCGAGGTGCAAGGCCATGCTCGGCGAGAGCACCGAGGAGC TGGCGGTGGCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132 C ...	...	CGCTGGTGCAGTACCGGGGAGGTGAGGOCATCTCGGCGAGAGCACCGAGGAGCTCGGGGTGG CCTCGCTCCACCTGCGCAAGCTGGTAAGCGCTCTCCGATGCCGATGACCTGCGAGAACCGCC TGGCAGTGTACAGGCGCGCGCGGAGGCGCGGAGGCGGCTCAGCGCATCCGCGAGGCGCTG GGGCGCTGTGGAAACAGGCGCGCTGGCGCGCGGCGGCTG
ESTD- ARSB	126 A ...	...	GGAGAAATGGAGCCTGTGGAGGAGGCGTCCGAGGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGTGGCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTGGACGTGGGAAACCATCAGTGAA GGAAGCCCATCCCCCAGAAATGAGCTGCTGCATAATTTGACCCCAAC
EST36770 4	144 C ...	...	TGTAGCCAAAGTCACCTGCATCATCTTGGCTGCTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTCTTCCATTATGATCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACTGGGTTTCTGTTTCTTCTGATCAT TCTACAAGTTTACTCTTATTGGAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137 A ...	...	TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGGTTGAGTGAGTGCATGTTGAAACCTGT CCATAAGTAATTTGTGAAGAGAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAATGA GCATTAGTACTTTTCAAGATTGAAGAGAAATGCATTTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTTGAACAAAGACAAAGCAAGGCC
ESTD- BA511	29 A/G ...	...	GGGCAACATAGTGAACCCCATCTCTACA/GJAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAAGCAAGATGGTGCCTGCA





ESTD- CB22	119 C T ---			GGCAAGTTTTATTGATAGAGAGGAAATCAAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCCCAACCCATAGGG[C/T]GGATACAAAG ACAGGAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCT AGTAACATAATTGTCITCAATTAATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---			TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATATGGTCTTTCGGGCTTCTCTCACACATACACAGAGCCCTACCAAGGACCAAGACAGCT CTCAGAGCAACCCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAAAACGTTTCCCAACCCGA GGTCGCTGTTTGAGCCATCAGAAGCAGATCTCCACACCCCAAA
ESTD- CB24	145 A ---			ACAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCCAACCGAGGTGCTGTGTTGAGCCATCAGAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCTGGCCACAGGCTTACCCCGACACAGTGGAGCTGAGTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGAGCAGACAGACCCCGAGCCCTCAAGGAG
ESTD- CB25	146 A G ---			GTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTCGCCGCT TCTGCTCTCGAACCCAGGGCATGGAAATCCACGGACACAGGGGCTGAGGAGGCCAGAGCCACCTG TGACAGGTTAG/CCTACATGCTCTGTTCTTGCAACAGAGCTTACCAGGAGGGTCTCTGCTGCC ACCATCCTCTATGAGATCTTGCTAGGGAGGGCCACCTTGATGCCGTG
ESTD- CB27	125 C T ---			TTTTCTGTTCCCTGAAGATTGAGTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGCTGGTTGCATTCAGGAGTGTCTGTGGAGTTCTGCTCATCACTGAC/C/TTATCTTC TGATTTAGGGAAGCAGCATCCCTTGGACATCTGAAGTGACAGCCCTTTCTCTCCACCCCAATGCT GCTTCTCTGTTCACTCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---			TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/ATATGTA TTTCTTAAACAATAAACTGAAAGTCCAAAATTAACCTTGATCCATGGAGTGCAGAAATAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGATATGTTCAATGAGCCCTTGGGTGACCAGGTGTA TTGCCAATAAGCAGTAATATTTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD- CYP2D6	61 A G ---			CAGCCAGCGTGTGAGGTGGTGCACCATCCCGGCAGAGAACAGGTAGCCACCCTATGCA/GC/A GGTCTCATCATTTGAAGCTGCTCAGGGTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---			AAAAAACATTTAACACCTTTCAATCATATACACATA/AVC/jatttttccatttttccacataagTCA GTTTGAGCTGAGTTTCCAAATTACTTGCAATCTAAAAATGTCATACTGATTAATGCAAGTTCAACAG ACAACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---			CATCCCAAGCCCATCTCTTAGCCACTGGCATTTTGGCGCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCATGGAAAGGCTCCTCTGGGGCGGTG GGGTGTGTGGCTATGTGGTGTCTGTGTAG/C/TJGGGGCTTTGGTTTCAGTTGCACTATTGGCTT ATTGCAAGTTGCTTGTCTTCCACCTGAGCGAGCCCTC

ESTD- D17S33a	75 C T ...	...	CATCCCCAAGCCCATCTCTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTAGGGCCGT CATGCTGCTACACATCCAGGGGGGCCCTACCCCTTTGTAGTCATGGAAAGGCTCCTCTGGGGCG GTGGGTGTGGCTATGTGGTGTCTGTGTAGACGGGGCTTTGGTTTTCAGTTGCATATTCGGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ...	...	TTTGAGACCACCTGGCCCAACATGGCGAAATCACATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGGAGGCTGAGGAGGAGAAITGCTTGAACCCJA /GJGAGGCAGAGCTTGAGTGAGCCCAAGATCACACCACCTGCACITACAGCCTGGGTGACACAGTGG GACTGCTGCTCAA
ESTD- D3S11	44 G ...	...	AACTGATTAGAACCTGAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTCATCATTAATAAATCCAATAAAGTACACTGTAATAAAGAAATTTAACAGAAATATCATTTGT TTATTCAAACTATTTATCACITATTTATTGTTAAGCCACTACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ...	...	AGGTTCCACATTAATGCTGATGTTTCTGATGTTTCJA/GJGAGGCTTGATGTCATCTGTATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTTATTAAATTCAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ...	...	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGTCAGGTTACAGCTGTATTCCTCC AGAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATACTGCTCTTTATTGGAAGGATGCTGCTGGT
ESTD- D3S2a	248 G ...	...	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGTCAGGTTACAGCTGTATTCCTCC AGAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATACTGCTCTTTATTGGAAGGATGCTGCTGGT
ESTD- D7S399	83 A G ...	...	TGAATCTTAATTGCTATCTACAAAATGTATAAATCCTGAACTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJA/GJGCTCTCTACATCATCTTTTCAAAACATTTTTCATCCATGGACTCCATAC TAGAATATTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ...	...	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTGGCCTCCACT TCCATGGGTGTGGGGCTGGGACCTCAGTCTCCCTGGGAGAGGAGGAGGTGGGAGGGAGACA GAATGCTGATTJA/CJTCTGGTGGAGAACCAACTTCTGGCCTGTGGGTAGGGGACGCTGCTCCAAAG ACCTCCTGATTTGAGGAAGGGGAGCAGAGCGAAGAACAGAGT
ESTD-DMa	66 C G ...	...	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTGGCCTCCACJ GJTTCCATGGGTGTGGGGCTGGGACCTCAGTCTCCCTGGGAGAGGAGGAGGTGGGAGGGAGAGA CAGAATGCTGATTATCTGTTGGAGAACCAACTTCTGGCCTGTGGGTAGGGGACGCTGCTTCCAAAGA CCTCCTGATTTGAGGAAGGGGAGCAGAGCGGAGAACAGAGT

-182-

ESTD- DRD1	154 C T ---	---	---	TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAGATCCACCCATCAC ACAAACGGTACAGACCCCAACCTCGAGATGAATCTGCCACACATGCTCATCCCAVAGCT AGAGGAGATTGCTCTGGGGC/TTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144 C ---	---	---	TCTGCCTTTGGTCAGAGGGCTGCCCGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGACCA GCCACCCGAGAGACCCGGTACAGCCCATCCACCCAGCCACACAGCTGACTCTCCCGACCCG TCCACACCGTCTCCACAGCACTCCACAGCCCGCCCAACACAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---	---	---	AAGACGATGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGATGTGGCGGGCTGGCTGG CACCTGTGGAGTTCTGCCCCACAGGTGTAGTTGAGGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTCTGTAGGAGA
ESTD- EPB82	93 C T ---	---	---	TCTTTCAGGATCCGATCTGCGCTGGTTGGGCATCGCTCCGCTAGGTGTACGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCAGTGC/TGGGGCGGGTGCAGACCCCGCTGGGAGGACTTCA CCCCGCTCACTCCGTTTCTGAGCAGTCTCCGCTCGTACT
ESTD- ETS2	43 A G ---	---	---	ACTCACAGTGTCTTTAAGTGAATGGTCGAGAAAGAGGACCA/GJGGAAGCCGCTCTGGCGCTG GCAGTCGTCGGACGGGATGTTCTGGCTGTTGAGATCTCAAGGAGCGAGCATGCTGTGGACACA CACAGACTATTTTGAATTTCTTTGCTTTTGCCTTTTGCACCGAGAACAGCAATGCAAAAACCTTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTCAGAAAGTTAGTTTG
ESTD-F9	111 A G ---	---	---	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTATAGATTTATGCCCA TGCTCCATTTTGTAGTTAATATTTGTGTAAGTATGATGTTTAA/GJGTCAAACTTCATTTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---	---	---	CTTCTATGGGATTTGACTTTATTTCTCAATGCTTACCTTTTACAGGTGTTAATATAGTGAAG GAAGCTTGCAGCTCATGACAATTTGAAGCTGACAATTACAAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAACATTGAAGTTGTTTGAACCTTGGTGTACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GDDH	200 C G ---	---	---	CCAGACCGGTGAGTGTGGGGTGGGAGTGTGGAGGAAGGAGGAACTGGGGGTTAGGGACT TTCCGGGGTGAATTTCCCGTTCTGTGCTTGACAGAGAAAGGGGGAGAACACAGAGCCCACTGGCTAA GTGTAAGGGAACCTCTGTGTCACCCGTGTGCTGCTGCCCTGTTCAGCTGTCTGTGCGCGAGT/C G/GACTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	88 A/G ---	---	---	GTTTTATGATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGCCACTCTCTGGTCAACCATGAC AACCACAGGCCCTCTCAGGA/GJACAGTAAGCCCTGGCAGGAGAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCAGCGGGCGCTGAGCCCCAGGAGGAGGCTAGGATGTGAGAGACACAGTCT ACCTGCAGCCTAATTACTCAAAGCTGTCCCCAGGTACAG

EST34088 2	62 A T ...			GTGGGGCAACAGTGGGAGAGAGAGGGGGCAGGGGTATAAAGGGGGCCACAAGAGACCGGCTC[M/T] AGGATCCCAAGGCCCAACTCCCGAACCACCTCAGGGTCTGTGGACAGCTACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ...			GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAC[AG/GG]CATCA TTGAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGATGTTCCCTAGG
ESTD-HT2	154 G ...			GGGTAAATTTCCGAGCACTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGACAGAGAGAAATAAAGGATAACCTGGGTTTCTGTGC TTTGCTTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT5	149 C ...			AACACAAAGCCCCAGCGAGAATTGAACCTCGGACCCCTGGTTTACAAACCAGTGCTTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTGTTTTCTTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCTCTACAAATGAAA ACATTTGCTGCTGTAAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ...			CTGAGAAACAATTGGCAATAAAGGAATTTGGCACTCCCCCCCCCTCTTCTCTCCCTTGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCCAGCAAGAGAAAGAG[AG/G]CCCCAGA AATCACAGGTGGGACGTCGCTGTCACGCCATCTCCCTTCACGGGAATTTTCAGGGTAAACT ACCCAGTGGAGCCCGCTCATTCGACCGTCTTGGCAGGAGTGCTCTGTGGGAGAAAGGAAGATG TTCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHBP1	43 C T ...			TTTACTATTTCAATGGATACAGAAATTGGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCCTACATTTGTTGAGTGACGGGGCAGTGGTGGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATAC TTCACAAATACTATAAACGGAGTTGAATATAAACCCCA
ESTD- IGHV4-6	120 C ...			CAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTATTATTATTATTATTTATTTTGT AGATGGAGTCTGGCTGTCAACCCAGGCTGGAGTGCAGTGGC[AG/G]CAATCTCGGCTCACTGCAAGCT CTGCCCTGGGTTCAATGCCATTCTCCCTCAGCTCCCGAGTAGCTGGGAATACAGGCAACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTACCCGT
ESTD-IL1A	110 A G ...			CCACTTACAGATGGAATAATGGGTACAATGAAGGGCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGCTCTACCTTGGGTGCTGTTCTCTGCCIC[AG/G]GAGCTCTCTGCAATTGCAGG
ESTD-IL1B	99 A G ...			TCCAGGTGGCTGACCCAGCCAGCCAGCTCTGCAGCAGGAGGAGCGTGGCTGGCTGGTGAAGCATG TGGGGGTGAGCCAGGGGCCCAAGGACGAGCGCACTGGCTTCAAGCTGCTCAGCCCTGCTGTC[AT/] TCCAGATCACTGCTCTCTGCCATGGCCCTGTGGATGGGCTCTGCCCTGCTGGGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGACGCTTTGTGAACCAACACCTGTGGC
EST74082	134 A T ...			

EST45311 0	151 C T	---	---	GGCCTCCTCTCTCCAAATCTGTCCCTATAGTTTTCCCTATTAAAGTGAACATGACATCTTTTAGT GGATAGATGCACACAAACACAAAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATC/TJACCTCTTTTCAATTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G	---	---	TGCCCCATACGCGCGGCGAGACATGGCTTGCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTCCJAGJCCCTCAAAATGACAGCCATGGCGCGCGGTCTTCTGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTTCATGGAGACTTGAGGAGGGAGGGCTTGAGGTTGGT GAGGTTAGGTGGGTCTTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	26 A T	---	---	ATGCAGGATGAAGGTGGACAGGGAGG/TJGAGGGCAACCTGTCAATCCAGGGCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149 G T	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCAATTTGTTTAGCATTAACCTAA TTTTTCTCCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTC/TJAGTGCCAGTATCCAGAGTTTTGGTTTTTGAAGTGAAGTGAAGTGAAGTGAAG AAGAACTGAATACCTAAGATTCTGCTTGGGTTTTTGGTGCAATGCA
ESTD- KRT10b	183 C T	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGC/TJTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAGTTTAAACCAGTATTGATA
ESTD- KRT10a	133 A G	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAT G/GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAGTTTAAACCAGTATTGATA
ESTD- KRT8b	231 C T	---	---	ACCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGAAATGTTAAGTACAAAGTGAAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCA/C/TJGTCAACATTGACACA
ESTD- KRT8a	21 C T	---	---	ACCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGAAATGTTAAGTACAAAGTGAAGGCCCAT GGCTGCCTATCTCTCCCGTCTCAGGTTTACCA/C/TJGTCAACATTGACACA
EST75099 6	82 C T	---	---	CACCTGTGTGTCTAGATCTCCTCAGTGGCGCCCTCTACTGGTTGACTCCAAACTTCACATCCATCA AGCATCGATGTCAAC/C/TJGGGGCAACCGGAAGACCATCTTGGAGGATGAAAGAGGCTGGCCCCACC CCTCTCCTGGCCGCTTTGAGGTGTTGG

ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAATTTGAACCGTAGCAAACTGCATTGGTATTTAGA AAAAATAAAAAATTTCCAATATGATGTGTGTTATACCTGCTCTGCCATGCAGCATCATAGCCTGT GGAAACC[A/G]GAGGGCTTCCCTTACCACCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGAGTTATTAGGCATGGTTACCTGTGATTTCCCAATCTTGCGTTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGCCACCGCTGTACCAATTAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCTCTGGAAGACAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD-LMP2	35 C G ---	---	TACACACTTCTTACCCATTCACTGAAAACGACT[C/G]GCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGCACCTCACCTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCTGCA AGGGTTTGTCTAATTTCAATTCAATGTCTCTCATCTTTAG[C/T]AGCTGTGGGTTTGTGTTG TTCTTCTGTTTTGCTTAGTATCTGACTACTTTTAAATATAAAAGAGATGATCTAAACAAAAATAG AGATTGTTATCAGAAGTTCAACAACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCCAGGAGTGTCTGATGCTGCCCTCCCGAGCTCTGCTCCAGG[C/T]GAACCTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTCCAAAGGTTGGTCTAAGTTGCTGATTAC[C/T]GGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGGTCTCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAAC[T/A/G]TACCAGATCCCACAGACTGATATGGCTGGT AAGATGGACTTGATATTTGTACAAAAAAAGTTTATTTTCTAAAAAAAGAAAAAGAGAAAA AAATTTAAAGGGTGACTTATATCCACACTGCACACTGCC[T/A/G]GCCCAAAACGTCTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTTGAAATCT GAGAAAACCTCTTTAAACCTCACCTTTGTGGGGTTTGGAGAAAGTTATCA
ESTD-NFKB1	107 A G ---	---	TGTCCTTAGGCCCCAGCCCTGCTTGTCTCCCTGGCTGTATCTT[C/A/G]GTACTGCAAGAGAACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATACTTTTGTTGTGATTATATATTAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGCTTGAATAGTAGATGCTTATTTAACCTTTGGCAATAGCATTTG C/TATTCCTGTGGTTTTTAATAAAT
ESTD-NRAS	202 C T ---	---	GCCACCAACCCACCAGCACACCTCCACCTCAGCCAGACAAGGTGTTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG[A/G]GTACGCCGTGTATCATCGAGCGGCCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTCTAGACAGACAAAACC TAGACAATCACGTGGCTGGCT
ESTD-PAH1	100 A G ---	---	





ESTD-TAT	224 C ---	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTCATCAGGGCCATCAGTTCATTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATCTAAATGACTTGTGGGACAGGATCA ATTTCTCTACCTAGAACGTTTGTACAACTTTCTCCAGTATGGATGGATTATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THPB	125 A C ---	---	---	TGGGCTTTCCTCGGCGAGGTAGACTTCTTACTTGGCTGTGATTTCOAAGAGAAAGAGTCCCAAG CACAGAAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATACAGAGATC/CJC/TTCAT CCACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAAGGTCGCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTGTCCCAAGCAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCCAGATTTCA/G/TATCCCCAA GCAGTGCATCCATTGACACATAATATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAA CATGGGTGTGATCCATTTTCAITTTGGCCATAGGTCCTATGGGGATGACA
ESTD-TYR	122 GT ---	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTGTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTTATGCAATTAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAG/C/JATTAAAGTTCTAGGCATCTT
ESTD- TYRP1	222 A C ---	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTGTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTTATGCAATTAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAG/C/JATTAAAGTTCTAGGCATCTT
ESTD- TYRP1	222 A C ---	---	---	TTCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGGCCCAAGACAAAGGTCACAGACAGGAAACACAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T ---	---	---	TTCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGGCCCAAGACAAAGGTCACAGACAGGAAACACAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	---	TTCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGGCCCAAGACAAAGGTCACAGACAGGAAACACAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGTTACAGGTGGCAGGCACAGCCAGTCCATCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGGAGAACAGGACAGCCACAGTGCGCGGGATGGCGCGGGAGTTC TGGTTGCGGCCACGGCTGGCCCTCGTTGTGAACGGTAGCCTTTGCGGTGCGATGCGCTAAACCTTTGT TTCTTGGCCAAAGGAGGGCGGGGTGCCATGCCCTGAGATGTAGATGGGOC
ESTD-VWF	36 G ---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTCCACACTGTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACACCTCTACGTCAAGCCTCAGCACCAGATGCTGTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCATGAAGAGCACAGAGATTATTTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCAGAGTACCAAGC/GTGTGTTGGTGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAAGAAAGGGCCATCCAAAG
ESTD- TNFAb	152 A G ---	---	TTCTGCATCTCTGTGGAAGTTAGAAAGAAACAGACACAGACCTGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGCATGAGGACGGGTTCAAGCTCCAGGTCTACACACAAATCAGTCAGTG GCCAGAGACCCCCCTCAGATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCTTTGATG CTGTGTGTCCTCAACTTCCAAATCCCCGCCCGCGGATGG
ESTD- TNFAa	88 A ---	---	TTCTGCATCTCTGTGGAAGTTAGAAAGAAACAGACACAGACCTGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGCATGAGGACGGGTTCAAGCTCCAGGTCTACACACAAATCAGTCAGTG GCCAGAGACCCCCCTCAGATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCTTTGATGCTT GTGTGTCCCCAACTTCCAAATCCCCGCCCGCGGATGG
EST52418 6	113 A G ---	---	CAATTACAGGGTCACTGCTATGATGTTTGGAGCCAGTCAACCTTTGGTGGCTACAAGATGTCG GGAGTGGCCGGGAGTTGGGCGAGTACGGGCTGCAGGCATACACTTAGTGAAGTGAACACTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTTGCCAGCCCCAGGACAGAGCTGATCCTTGAACCTTAAGTTCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAG/GGGCTGGCTTATCAGCCTCCAGCCAGCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCSGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAAACTGGGCCCCCATGGGGGACGTGGAAAGCCACTTGAGCTTCTCTGGAGAGGACCTGA GGGACAAGGTCAACTCTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAGAGTCTCTCTC CTTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGGAGGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTGGTAGTCCAGTGTGACTCATCCAAATGATTTCTCCAGTGTCTGTTCTCGAGTTTT CTCTGCCATGTTGCTATTGAGGACGGACCTGTCCCAGCCAGATGATTTACCATTTCCACAGTGGT CCC/GJTAAAAACATTCTATGAGCCAGGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTG TCCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	---	AGACCTCAGTTTCTCTGTGTAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGCCTTAGCA CTGTGCCCTGTAGTCTGTATCAGGTAGAGGAGATGGACACAGGTGGAGAGAAATTTGAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAAAGAGCTGGGAAATGTGG
EST39852 8	106 C G ---	---	---	CGGTCTTCCATCCAGGTATTGTGCAGAAAGGCCGAGATGACCTCTATGTCTCAGATGCATCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTA[C/G]GTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAAGGCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	---	ACCTGGTGTGCTGGTGTGGTGAACCTGTCTCTTGGCATTGCCGGCCCTCTCTGGGCGCCGTGG TCCTCCTGGTGTGGTAGTCTGGAGTCAACGGTCTCTT[AG/G]GTGAAGCTGGTCTGATGGCA ACCCTGGGAACGATGGTCCGCCAGGTCCGATGGTCAACCGGACACAAGGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	---	AGTGACTTCCAAGGAATGGCTACCCAACTTGCCTTCATGGCCCTGTGGCCAACTATGCTCTCAGA ACATACCTACCCTGCAAGAACAGCATTTGCATACATGGATGAGGAGACTGG[AG/CAACCTGAAAA AGGCTGTCACTTACAGGGCTCTAATGATGTTGAACCTTGTCTGAGGGCAACAGAGGTTTCACTTAC ACTGTTCTGTAGATGGCTGCTCTAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCTCTGCTCACTT[CA/G]GGGTTCAGAGTGGAAAA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAACA[C/TT]GGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAAATTTTATTGACCAACACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	---	GCCGAATGCCCGGAGTTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGTATGCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCCTCTCATCATGAAAAAC TGGGAGGCCGGGCAT[AG/G]GTGCTCATGCCTGTAAATCCAGCATTTTGAAGGGCTGAGGCGGGTGGAT CACTTGAGGTGAGGAGTTTGAACCAACCTGGCCCAACAT
EST12274 0	135 A G ---	---	---	CCCCAGTTGACAGCCACTGCTAGACTAAGTTTCTTGGCTTCCAAATAGAGCCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACTCCTCATGACCAATAATCTTCCCTCCCTTAGGATGAGGTG[ A/G]TAGTAATGACCGATGGGTGAGAACTGTTCTGTGTCACCATGGAGGATACTATAACTGTGAAGA TAAATCAAGCCACAGAGCTTGCAGATC
EST76807	91 G ---	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCCTATCTCCAGGGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAAGGCCAGGCACTGGGCTCCGAGGACTCAACCACTGCCOCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T	---	---	TTACATTTGGGATGTTTCTTTTGGCTGTCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAGTTTGGCTTGGCTGCCTGTGGGATATTTGAAGAGATGCTTTGGCAGTCCCAATGCTCTAGAGATTTGCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCTTAGATTI/MGTCTTTAATCCATTTGATTTGATTCTGTGA
ESTD-FYR1	109 A G	---	---	CTTCGTGACGGGAGGTCAGTCTCCGCTCTTTTCATGGACATATGGATGATGCTGACCATTTCCCCTGCTGACAGTATGACAGCGCAGACTTGTCTACTATAGAGI/GJGGGAGCTGTGTGCACTAIGCCCGCTCCCTCTGGAGGCTGGAGCCACTGAGAACTAGCTGGAGTGGGAGCCACCTGGCTGGGGCCAGCCACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCTGCAAGATGTGCGI/GJCGTGTGCTGGAGTAGCCCCGACTCTTGTACGGTGGCATCTGAGACCAGTGAGAAACGCCCTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCTGCACCAATGGCTCCAAAGCCCGTAGGGAACTGGGGGATCTAGGGGATGGGTGAGGAATGGGCGCAGCCAGTCCGGCGGTGCTGGGTCCCAACAGAGAGGCGGTGGAGGAGACAGAGATGGGCTGGATGAG
ESTD-PBDA	103 A G	---	---	GCAGCCAGGAGCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGAIC/TJGTCTGTCTCCGACCTAAGCGGAGCAGCCCTCAAGAGCCGAGCGGAGTGGG
EST12839 3	122 A G	---	---	CCCTTCATGCCCCAGATGGAAATTCAGTCCCTTCAGGATCTGCCTACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAAI/GJCTCTACCCGAGCTTGTCTGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G	---	---	TGCAAAACACACAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTGGCTCCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGI/GJTCAAAGTCCAAGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACITGAATGTTATTCAAC
ESTD-ACE	96 C T	---	---	TGGATTTCCAGTAGGTTTCAGTTTACTTATGAATATTATGATACCTTAGCTTAG
EST54419 8	88 A G	---	---	ATGGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTI/GJCCAGGACCTGGCCCTGCACCTCCTGTTTTTCTCTCTTCATCCCTGTCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGTACTGGCCAGCAGCGGAGGCATCGCCAGCTTTGTGTGTGATGATGCAITCTCCAGGCAAGCCAC
				GATCAAGCAGTGCACACGGGTCACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGAGTACAAGGATCTGCCI/GJGTCTCCCTGCGTGGGGGGCCAAACCCCGGCTTCCA
				TGAGGCCATTGGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGAACATCTGCACAAATCGGCGCTGCCTTCGCTAAATTTGAATGATATTGTGTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTATTTCTTGACCCCTACTTACI/GJATCCTGGGAGATGATTTGGGTTTAGCGTGGTGTGATGTTGTCTACTATAGTCCCAAGTGAA

ESTD-PS-1	99 A G ---	---	---	GGGAGTAAACTTGGATTGGAGATTTCATTTTACAGTGTCTGGTTGGTAAAGCCCTCAGCAMCA GCCAGTGGAGACTGGAAACACACCATAGCCTAGJTTCGTAGCCATATTAAITGGTTTGTGGCTTAC ATTATTACTCCTTGGCAATTTTCAGAAAGCATGGCAGCTCTCCAATCTCCATCACCCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	---	GGCTGCCAGGGTTCGTGGAGCGCGCCCTAGCCGGGCGCTGGCGCTGGCGGTGGCTGGCCACC GTGGAGGCAACCTGCTGGTCACTGTGGCCATCGCCCTGAGACTCCAGAGACTCCAGACCATTGACCAA CGTGTCTGTGACTTGGCTGGCCGCGAGCCGACTGGTGTGGGACTCCTGGTGGCGCGCGCGGCGCA CCTGGGCG
WI-567b	48 A G ---	---	---	TCTACACTGACCCCTACCTTCATCCTCACCTCTGCTGCCCTGGTTCTAGAGCCCTCATCTCTTTA CAGGATCCGCCACAGATCCCACTGATCTGGCCTTAGGCTCTCTCTCCAAATCCATCTTCAAAAG GCTGCCACTGTGATCTCCCAAAGGTGATTCTGATGCTACCATTCTGCTTCAAGCC
WI-801c	58 G T ---	---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTGTGTAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGACGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCAACAGAGATTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---	---	---	ATGMAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTGTGTAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGACGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCAACAGAGATTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	---	GAATTCACCTATACAAGAACTATTTCTCTAATTATTTACATTAGTCTCATTATCTGAAATATTAT TTTTTACAAGTACCTTTGATTATTTTGTATTCATTTGTAACGAGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTGTATCACAATGTCTAAATACTTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTA
WI-2529	71 C T ---	---	---	AGGAAATGGCTGATCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA/C/TCTTAAGTCTGCTTCAAGTCAAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAAGATCATTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-1008b	205 C G ---	---	---	TAAGGGCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACATATAGAGAGACCTGTACCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG/C/GIAGCAGAAAGCAGCAAGGAGGAGAAAGGAAGT

WI-2625	98 G A ---	---	---	GGG CAG T C C T G G C T G A G T G G T A G A C A G C A C T G A A G G A T G G A G A G A G A A A A C A G G C A G A A G C A C T G T G T A G T T A A C A A G G C T T A T T A G G A [G/A] C A A A T T G A T A C T C C C T G A G G A C T C G C A G A A T T A C C A G C A G T G A C A G G T T A T C T G T G G T G A A T T C A G T T A T T C C A C T T G C A G G A G A A A G C C A G C C A A A G
WI-2924	54 G A T A G G	T G A C C T T C C T A	G C C C T A A G T G T	T C T G T T G T C A T A T T C C C T C T T T G A C T G T G A C C T T C C T A G C T T C T C T T A T A G G [G/A] A C C C T G T G A T T A C A C T T A G G C C T A C C T G G A T T A T T A G A C A A T C
WI-2939	72 G T G T G C C T T T	G G C T T G T C T C A	C T T G T T G A G G G	C C A T T G T G A G G T G G G T G G G T C A C T T G T C A T T C C C T G C A C T C A C A A A G T G G C T T G T C A G T G C C T T T [G/T] C A A G A C C T T C C C T C A A C A A G A A T G T C T T T C C A T G C T C C C G T G T C T T T G A A A A T T C G A C T T A T C C T G A A A A A C T A G C T G C A G T G T T A T C T C C G G T A T A A G C C A C T C C T G
WI-3203	99 G A A G A C G A G	G G T T A T G C G C	T C A A G T A T T G C	C T T G C T A C C A T T C A C A G C A T A C A C C C T C A G T G A A T G C C G T A A C C C C A T T A T A A A C A T C T T G C C A T C G A A G G G T T A T G C C G A G A C G A G [G/A] C C A C A C A A G G C A A T A C T T G A A G T A C T T G G A G A A A G A T T T T G G A T G G A T G A A G C A G A G A G A T G C T A A A A G T G A
WI-3473	101 A G G C C T A G G G A	A A G C A T T T T A	C C T G A T G T C A C	G G A A A A A C C T G A A G G A T G A T A G A A G T T A A T T G G G A G A T A G T T G G T A T A G G C C C T G T T T G G A G A T T G C A G A G A A G G A A G C A T T T A G C C T A G G G A [G/T] A G A A A A T T G T G T G A C A T C A G G G C T
WI-1796b	29 A G ---	---	---	A C A C A C T T T T C T G T A T G C T C T T C A T C A A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T A A G C A G G A G C A T T G T C T T G C T C C C C
WI-1796	29 A G ---	---	---	A C A C A C T T T T C T G T A T G C T C T T C A T C A A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T A A G C A G G A G C A T T G T C T T G C T C C C C
WI-4360	93 C T A A A T A A	G T A G T C A C A T T	G A G A T A T T T	A G T C G T C C A T C T T C A G G G T C T A A C T C T G G A T C T G C C C T G C A G A G T A G G A A A A G A A G A T G G G T G A G T A G T C A C A T T A G G T A T T T C C A A A T A A [C/T] A A A A T G C C T C T G A A A A A T A C T C C C A T G T C C C T G T C T A A A T A A C A T T T T C C C
WI-1959b	87 C T ---	---	---	G C T G A G C T T T G T G C A G A G C C A G G G A C A A T T C A G C T G C C G A T T T T A T A G A T T C T G C A G C A C T G C A A C A G G A C C A A A A T C A G T C [C/T] G G G T A A C T G A G A G T G G T T T T C A C A C C C A A A
WI-1973b	28 A G ---	---	---	G T T G T C C C T G T A G C A G A C A G A A G G C A [A/G] A G A G G A A A A A G C C T T T T T G T C C A G G G G C T T A C A C T G A A T C C C C T C A A A C A A T G C A A G A T G A G C T A A T G G T C T T A G A G G T A T A A T C T A A G T G T G A G A A A A C A A A A G G T A T A G G G T T G
WI-1980b	140 C T ---	---	---	C T T G A G T A T G C T G G A T T T T G G T A T A C A G A A A T G G G A G A G C T G G A C T A A T C C C C C C A T A T A C C A A G G A C A A A T T G T A T C T G T T C T A C A A T T A C A G T A G G A G A C A T A T G T T C C A T G A C A A T G G T A A T T T T A A [C/T] G A C A G T T T T A A T T G A G T G A A A T T A C C A T A A A A A T A A T A A T A G T A G C A G C T A A T A T T T A C T G A G C T G T T A C T A G G T G C C T A T A A A T A G C

WI-2015b	190 A G ---			TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAATATACAAATTACTTGACAGATAGCATGACCAATGCTAGTGAACCCACACAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGTCTTTTCCAACT[A/G]CATATACCTT CTAATACCATAGAG
WI-754b	49 C T ---			GAAGGCACAGGAGAGAGATGGCTGTCATCTACCAGCCAGGAGAGAGAGC[CT]ACATTTATTGGTAA TCCTATAAAGTGCATTCTTTAAAAATTTGTATTACTTTAGA
WI-754	22 T C ---			GAAGGCACAGGAGAGAGATGGC[CT]GTCATCTACCAGCCAGGAGAGAGAGCCACATTTATTGGTAA TCCTATAAAGTGCATTCTTTAAAAATTTGTATTACTTTAGA
WIR-1b	56 A G ---			AGGCAATCAGACCTACAGAGAGAAACCCCAATAAAACTCTGATGATCGTACATCC[A/G]TGCGCTG GAGGTGATGCTCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56 A G ---			AGGCAATCAGACCTACAGAGAGAAACCCCAATAAAACTCTGATGATCGTACATCC[A/G]TGCGCTG GAGGTGATGCTCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72 A G ---			TAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT[A/G]TCTAAAGTTATTAGTCAGAGCCCTCACACATTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---			TAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA[A/G]TATCTAAAGTTATTAGTCAGAGCCCTCACACATTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---			GAGCCTTTCTAAATTAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209 C ---			CGGGACAGAGACAGACAGAGAGAGTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACACAGG TTTACGTCCAG
WIR-5f	196 C ---			CGGGACAGAGACAGACAGAGAGTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACACAGG TTTACGTCCAG
WIR-5e	194 C ---			CGGGACAGAGACAGACAGAGAGTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACACAGG TTTACGTCCAG

WIR-5d	191 A	---	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAGG TTTACGTCCAG
WIR-5c	177 C	---	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAGG TTTACGTCCAG
WIR-5b	159 A	---	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGTGT AGGTTTGAAGGGAAGGCAAGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACAC AGGTTTACGTCCAG
WIR-5a	37 A G	---	---	---	TAACCTGAAACTTGTCTCTCATCTCAGGGGAGAACACAGACTTCATGTTAAGACCCAGAA[AC] CCAGCTTGGGTTGGGCGAG
WIR-6	63 A C	---	---	---	TTCTGACTATTCTAAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C T	---	---	---	GGGTCTCTATGACTATCTGTCGTCATTGATTGACTAATGATTCCTGCTGGCCCTTG
WIR-8	46 C T	---	---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAGTTGTCAGAAAGAGGTATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATAACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAC
WIR-2	56 C G	---	---	---	TGTCCTTGCTTATGCCTGCTCTTTGCGCTTGGCAGGATGCTGTCATTAGTATTTCACAAGAAGTA GCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCATGCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTTGTTCAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCAGTC
WI-7069	93 G A	---	---	---	GGTCATTTCTTTTATCTGTCAGGAGCCAGCTCTGACTT[A/T]CTCTCTGTTCTGTCATCTCTCCC CCACATACCAACTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATAGGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A T	---	---	---	CCTATATTCA AGTTTGGAAA
WI-18612	37 A G T G C	---	---	---	TTGATTTGCTG CTTGCAAAT
					CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]ATTTCGAAGCAGCAATACAAAAAGTA TTTATGAAGAATGCATAATCTCTGAAAATTATGAAACATCCCT



WI-18517	87	C	T	CAGCTGA	CAGGAATCAG	TGTTTGG/CAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTGTGTCAACTCTACAGCCCTGCATGCC ACAGGAATCAGCAGCCTGAG/CTGTGTGACATGTGCCAAACACAACTG/CTGC
WI-18668	76	C	T	TAGGCAAAA	GGCGAAAAAC	GCTAAAATTAAA CTGCACATTTT GC	CGATTGACAACCTTTATTTTCAACTTAGTAACAGTCCAAATCAGGTAGATTGGCGAAAAACT AGGCAAAAAC/CTAGCAAAAAGTGCAGTTTAAATTTAGCAAGGCTCAAGACAGATGTGGAAGGAA GGTGAGATTTCCCTCTACT
WI-18680	75	T	C	A	AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATAGGAGTACTGTACAAGCAAGCATGATCCCTGAGTCTGAGTGGCTGTCACTCTAGC ATCTGGAAT/CTGCTCGGTTGTATATTCAGGAGGGGA
WI-18704	99	A	C	GGGGTAC	GGGTCTCCGA	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTGTGGAGCACCACACCAAGGCGAGGTTGGCTTGAAGGAGCC CTTGAGGAACACCGGTTCTCGAGGGGTAC/CTCCAGCAGGGCTTCAGCTTAAAGTCG
WI-18673	29	A	G	---	---	---	TGTGGCAAAACCTTGTTTTAATTTGCAAAAC/AGTCTTAAATTTACAGCATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTACATATGAATATATAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T	C	G333	GTGCTGGGGT	GCAAAATACCAC TGAAGAGGAC A	ACCAGTCACTTTTATTTGAGGTTAATTCCTATTAGGATATGAAGGATTCAGCAACGATTGAGATT GTGCTCTACGGAGGGCTCGGGCCAAAGTGTGGGGTGGGGGTGCAGAGT/CTGTGCTCTTC AGTGGTATTTGGGAGC
WI-18533b	91	T	C	---	---	---	GGGGAGAGGAGGTAGATTGCCAAATGAGGCAATTTTAAACTCCCGAGATTTCCTCTTTATT TATATTTCAATTTTCATCTTAAT/CTTACAGGCAATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T	G	---	---	---	GGGGAGAGGAGGTAGATTGCCAAATGAGGCAATTTTAACTCCCGAGATTTCCTCTTTA TTTTATATTTCAATTTTCATCTTAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A	C	TTC	TCATCTGATAC CTTGTTTCAGAT	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGCAAGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTTTTCATCTGATA CCTTGTTTCAGATTG/CTAAATAGTTGTAGCCTTATCTGTTTACAGATGTGAACCTTT
D49493	159	A	T	CTGGGAATT	CCTGAAGGAA	ACTTTCAGGCC AGGGC	CAGGACTTGTTGCTGAGCTGCAGACACAGAGCAGCTCATGGGCAACATCACTGGGGCCACAGAG AGCTGTCCGCCAGTGCATCATTAGGGGTCTTTTCACTGTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATTT/CTGGCCTGGCCTGAAAGTGGCCCATCATCATCCCACTGTT CT
EST10030	7	T	C	CTCAAGTCCC	CATTTTGTTC	GCAGTGGTGGT ATGGATGA	TATTTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCAGCACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCT/CTCATCCATACCACCACTGCTGATTTG
EST10052	2	G	A	GAGGCTG	GCTCACTCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTCTGAGGCTG/CTAAAGTCTAAGATTGAGGTTCCACATCTTTGTGAGGGCTTC CTGTTGAGTCAATAACCTGGTGGGAAGTCACTCATGTGGCAAGAGAGAGGCTACAGAGCAAGAGGAA A

EST10605 2	118 C G ...	CTCTCAAGTAG ATAAGAGGCA TAATCT	... GCTAAATTTTC AGAAAGAAATT TTGTTT	CTTGGTAAATCACAGTTCTGTATTATACAAAAAAGTTGTTTCTCTGACAAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G	ATAAGAGGCA TAATCT	AGAAAGAAATT TTGTTT	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT[G/JAA ACAAATTTCTTTCTGAAATTTAGCTTATGAACCTATTACACTGCAACCCAGAGAGGAGCAC TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAATGAAG[G/JGGAAATGAAGGCAATATCAGATAAA
EST11260 8	101 G T	...	...	TTGATGGAGAAATCCGAGGCTGCCAGCATCCCCACAGTAGATTCTTTGGACGAAGAAATCCT TCTGTGGATTGAGCTTTACCGCTTTTCTCTCATCTGCTGGT[G/C]TTTCTCTCAGAGCTTTAATGTCCGT CCGTCTCTCGAGTCAG
EST11349 9	109 C T	...	...	GAATTCGGGTATTAAATAGCGGGTGCCACAGGAGCACATAGGAAGAGCATCCAACTACTTTGGAG CCCT[NGJAGGAGTTTTAGAGAAAGCTGGAGCCGGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGGA
WI- 16632a	71 A G	CCAACTACTT TGGAGCCCT	CTAAAACTCC T	CCAGGAATAAAAGAAAAAGAGTCAGAGGAACACAGCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[AGJGACTATTTCTTCTGACTATAAGTGATGAATAAATACATTGAAGACTTTCAGGAGCTCA CTTGCCATTATTTTGTGCATGTTGTTCTTAAAGGCTTGTAAGAGATACTTGAATGTGGGAAC ACATAGATCCCAG[AGJATTAAGGGGCTGGAAGT/GCCTTAAGAC
EST11772 6	74 A G	...	...	AGAGCAATGGTGGCATCTCAATAAGCAGCTCATTTTGATTAC[AGJGGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAGCCCTCCACAGAACTTCATGCACCCTGAGCTATGTGAAC TGAAAGTAACAGTGGGAT
EST11795 3	82 G A	CAATAAGCAG CTCATTTTGAT TAC	ACTTCATGAAT TTTACTTCATG TATACC	GCCTAGTAATCCAAAAGGAACATGTTTGTATATAACACTCACTACAAAGTCTGT[AGJATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC GTGGAAAAATTTTATCTGTACGCTTTTCC[CT/CJATTATATTTAICTTGTCCCTGATTTTCAGCACCC CACCCGATTTGAGCAGTGTCTTTCTAAACTGTGCCCTGTGAGCTGTAAAGTCTTCT
WI-16644 42	42 G A	CAATAAGCAG CTCATTTTGAT TAC	ACTTCATGAAT TTTACTTCATG TATACC	CCCCTAGCAATGACTTGGAGTTGTGTCCTCAATTACCAAGTTACATCTGTTGCCAAAATTAAAGCTCTC TTCCCAGAGGCATTAACTGAGATTAT[AGJGGAAACGCACAGCAAAATTGACGATGCAGCTTTTTTA CCTTTTTA
EST12005 9	56 A G	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TCTGGAT	ATCTTGAGGTTTCTGGGCCCTGTCAG[NGJAGGTGACATCTTTTACTTACACAGGTCAGGAACCCCTAT AAAGAAACTGTGTAGAAAAGATATCAGGTCAGACTTTTTTAAAGGGCTCTTATCAGCTCAATAAA
EST12055 9	32 T C	...	...	
EST12492 1b	95 A G	...	...	
EST12492 4	25 A G	...	...	

EST12502 2	52 C G ---			ATACTAGGGAGAAACCAACTGGAGGCAAGTCCACAGGTCACACTGTCAIC/G/CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAATGCTACGGGGAAATGACCATTTTAAAGGCCATGTG GTGCTCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAAATGATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTACAAA CAGGTGTTTATTATCCCAATGACAGTGTGCTGAGAT/C/GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTTCAATTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCACCCGGC/A /GTTGAGAATACAATATTGAAGAAGAGTCACTGCCTGCCCTGTGGAATAATCAGAGTATTTGA
EST12817 9a	22 C A ---			TTGGGGTCTCCAGGATTCAG/C/ACTGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCAGGG GTTCITGGGAGTGACCGGATCCGGAATCCATGTGCTTGGGTACTCCATCAGGTCATTGGG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCCTGCA/T/AACACAGCCAGTTATTCACCAGAAATTTGTTGGGTTTCA ATGTAGTGTAGCTTTAATACACTGCACCTGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGCTCCTGT GGGCTC	AGGATTTTCATGAGGCTTTAATCATACCTAATAATACTGTTAAAAACAACAC/A/GTCTGTCACTTG CAGAGACCCACAGGAGACACATTCCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTGTTTTCTTAATGAAGCATATAAAGAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA/C/TGGAGCAGAAGCAGCTTCCCACCCCAAG CACCTCTGAAC
EST13117 6	66 A G ---			TGCTGTGTCATCAGTCCCTTTAAAAATTTAATCGCTTTATACAAATTGACACCAATAAATGCAC/A /G/TATTTAAAGTTTACAATTTGAGAAGCTGACACGTTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC/C/TAGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTTCTGTGTGTGCGAGGCCAGTCTCCTCACTGTCCTCATGAATAGCC AGCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGTGCTTTAATTTGAAAAGCATTGAGGAAATAAATTAATGAAATAGTCT GGCCATT/T/G/GACTAACCCAGTTCTACAAATTCACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTGCGCGTCAATATGCAGCTCAGATGTGAGAG ACGC/GATCTCTGTACAGGAGCGGCTACTGTCTTCAATCCTTTGCATGACAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAGATTT	ACAAGAGGGTT TGACAAAAGA	AAAGATATAAAAAACACTCCCATCAGTAGCAATACAAGGTTATACATTTTAAACCAGATTTTCTCAGG CC/T/C/TTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCCTCTTGATATAACCA

EST13278 2a	51 A G G	CTTACCGAA CAATATTTAG G	CATATCTGG GTGGTGAGAA	TTGCGAAGACGTTTACAGCTCCAAACCTTTACCGAACAATATTTTAGG[A/G]ATTTGAAATAT TTCTGTAGTTCTACCAACCCCAAGATATGACAGCTTG
EST13282 0	99 A T	AGTCCAAGA	CCACACATTTG GATGGAAATTT TGAGGAAGGTT	GCTCACTAGATGAGCAATTGACCAAAATATTTAGATAATACCTGTGGGAAAGTGGTGAATTAAGCC TGCCTGAGAATCCCAACACATTTGAGTCCAAG[A/T]AACCTTCCCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39 A G CTT	CAATTTTGA AGTTGGGTT	AAATCACTTCA TGGAAATTTCA G	AGCTCATCTGCAAGCAATTTTGAAGTTTGGGTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGTGGCTTTTGG
EST13518 2	45 C G	---	---	GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTCAGCATTTA[C/G]ACTTTTAAATTAACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGACCTTCCTTATAACCTTGATTG
EST13522 8a	66 A G	---	---	CAGGTTGGTGAATCTCAACTAGGAGCTATTTGCCCCCATCCCCACCCGCGCAGTGTCTGGAGAC[A/ G]GTTTGTATGTCACAACTGCGAGAGGTTGGTCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C	---	---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGAGAAAGGAGGTTCCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G	---	---	AAGATTACGGACCATAGAAGTCTGCCCCCGACCCATACACACAATTTATAGCAGGTAAACCAA CTGAAAGGAACAAGTAATGACTTCTTGAACAA[C/G]GATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G	---	---	CCTCAACCATCTGTAACCCGAGCC[A/G]CAGTGACCCGGGACTTGCTGCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGGTCAGTCAGCAGGTG
EST14083 7	23 A G	---	---	CAATGGTGTCCTCATGTGAACATAT[A/G]ACCTATTTCATAAAGTTAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGAACGACAGGAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	AATATCAATGCATCTTGTTGGCATGCTAGACAGAGGCAATAT[C/G]TTTGAAGATCTTTTAAAAAT ATTTTGACTTGTTCCCTTACACTCATTTTAAATGT
EST14812 2	50 A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTTAC TTAAATCCCAT TAATGACT	TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATTTCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAATCTTTAGAGTCCCGGAGTTGCCCTTTCTAACATTTTCATATCAGGTGAAAAAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T	CATCACCCACG ATACTGGTT	CGGGAANAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCGCTCTCCCACTGAACCAAGTAAT TCACACAGACAATGGCGCACCACTTAAATAAACTTGCCCGTCAACCCCACTACTGGTT[A/T]TTCC GGTACTGTTTTCGGTA

EST15420 6	109	C A	---	---	TTTAAACCCCAAGACTGTAGATGTCAGGACITCCGATCATTTTCTCTGCTATAGCTTGGATATCTTA ATCTCCGCTTTGTCATCATATAATCATATAGCCAAGGACTC/AJGGAATTTTGGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48	G C	GGA	GAATAGCTGA AACAGAGATA TTATTCTC	GTCACCAGCACATTTTATTAGACGTGAAAGACAAAGACACAGAGAG/CJAGCAGAGAATAATA TCCTGTTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57	G A	CACAAGC	GATAGTTGATG TTCATTATTCC CTATAA	AAGGATTGAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAAGC/GAJTTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGCCAAATGGCTCCCAAGGT
WI-16782	96	C T	CACGTAAAGG	CTTCTATCTTT CTGTCTCTCCA TC	CTTCTCTCTCTAGACGTGGAATACACACGAGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAGG/CJTGATGGAGGACACAGAAAGATAGAAGAGTTTGGGGT GCTGATGAAATTTGGGG
WI-16783	64	A G	G	CTGCTTGGTTC AATCCTTATTA G	AAAAATGTAAACCTTAGAGGTGGCTCTTTTGTGTCACCTTTTCTGAGATGCTTTTACCTGAG/GJ CTAATAAGGATTGAACCAAGCAGATATTTTAAATGGCAAAAGTCCAGATGTAACCTGAGT
EST15948 2	58	T C	---	---	CAGGACTTAAGGTCAATTTTGCCTGGAAGACTTAACTAAAGGTCAGGGCAACATAGGAT/CJTGTA CAGCACCACTCGGACAGGAGTCTGCTGAAATCGTCACACTAGCGTGGCCAGCCCTTTTCTCTGGC TGCTCTGCTCCAGAGC
EST16088 8	89	G C	---	---	GGTTTGAAGACGCAGCTTATCTCCACCTGCCACTGGGATTCATTTTGAGAGCTGTTTGTGACGC TTTCCAGAAAGGCCGCTC/GCJGGGTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96	C T	---	---	CGTCTGAAGTTTCTTTATCACAAAGTCACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTC CTGAAAGCCATCCCTAAGTAGTCTCTC/CJAAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24	C G	---	---	ATCCCAGCTGTGAAGGACAGGAG/CJGJTAACACACAGTCCATTTATAAGGGGTGTCACATTCCCA GGGGTCCAAATATGCAACATTTTCACTCGTCCATGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTGGCTC
EST16104 9a	83	A G	---	---	TTCCTTTAAATAACCCACAGACACCCCATGACACTTCCAAATTTACAGAGCAAAAGATTTGCAG CTGGTTCTCCAGGGA/GJTTGGCCCCGAGGCTGGCTCAGTTTCACTCCAGGACCTCAGTC
EST16118 0b	119	T C	---	---	ATGGTATAACAAATCAGTTCAGGTTTTTTTTCGTAACAAATGATCCTTTGGTCTTTCCCGTGGC CTCCTAAACAACTAAACAAACCCCTACGTCTAATCAGTCACTAACGATATCGAGTGGCAAGT CTTTCACA
EST16118 0a	32	C G	---	---	ATGGTATAACAAATCAGTTCAGGTTTTTTTTCGJTAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCTAAACAACTAAACAAACCCCTACGTCTAATCAGTCACTAACGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 CT ---			AGCCAAITCAAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGATTAC/TAATGAACGT AAATAATTCAGGGAATTTTGATCTAAAGCATTTTGCTTAGCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 GA ---			CATTGTTGGGTAGGGAAAGATAGTAGTGCAATAAAATGGTAAACAGCAG/GA/AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAAATTTATTACTGAGGGTGATAGGCAGAAGTAGTA
EST16183 2b	59 AG ---			GCAGGTAACACTGGTTCACAACTGTTCTTCATATAAGAAAGAAATATCTAGTTG/GAGTAG AGGAAGGCACTGCTCTCCGCGCTTCCTGTCATATTTTATGTCACGTGCTCCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 GA ---			AATCTTAGGCTCTTGGCTTTCAAATCA/G/ATACAGACAGATAAGAGCTTTAAGTATTTGCAATTT CCCCAGAGGAAAAGTCAGCATATAAACACATGGTCACTCAGGCACATGGTGTC
EST16229 2c	52 TC ---			TGTGAACTCGAATTGCTTGTCCAAGTCCCTGAGTCACAGTTTCATTTGGGAGT/C/CCCTGTGCAGCC CTTGCCAGTTTCCAGAGGAGGATACCTCAGCTAGCTGATTCAGACAGGAGGCTGCA
EST16229 2b	45 TC ---			TGTGAACTCGAATTGCTTGTCCAAGTCCCTGAGTCACAGTTTCATTTGTTGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCAGAGGAGGATACCTCAGCTAGCTGATTCAGACAGGAGGCTGCA
WI-16816	124 AG TGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTTCCCTCACACCTCATTTGGCTGGAACTGGGTACATGCACATCCTTGAACATATCATTTGGCAA AGGGAATGGGTACATAAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA/G/ACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49 GA ---			GCCACTCTCCTGTGGCTTGTCTCTGTCAGCTGCTGCCAGTGCCACAG/ATGGTGTAGCCTCATGG CAGAAGCATTTTAGCCAACTCCTGGTGTCTGCTCCACTCTCTCTCTCCGCCGCTGGGCTCACCACC TCTTCTCCTCAATC
WI-16824b	83 GA ---			GTCACCCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTTGG/GA/CTTACACCTTTAGCACGGATAGTTTCTGTTGCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 TC CAGCTGT	TGATGGTGTG	TCTTCATAAG	GTCACCCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTTGTTCTTATGAAGAAGTC AGAAGCTGATAAACGTTGGGCTTACACCTTAGCACGGATAGTTTCTGTTGCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 TC ---			TTGCTTTTATTAAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTTATTCATTACAAA AATGGCTTCCAAACCATTTAAATGAACCTT/C/GGAATAAGAGCATAAACGGAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA	TGTGAATTGGG	TATAATCCATCTCCAACACACACACAAATAAGCAGTAATGGCAATG/A/CTAGTGGTCTTCCCAA TTCAAGACCTGTGCTTCAAATTTTCTGATAATGTGGAGAAATCTGCTCTTTATGTA

WI-16879	79 C T	GATACAGGCC ATAATTTCCCA CC	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCACTATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCCACCCAG
WI-16882	99 A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGTGGGAGAGACAATCTCCCTTTACCCCAAAGGTTACTCTGAC AAGGCTATGAATGAATGCCACGTCTCTGAC/GJGGGATTAACCTGACATGTCATCTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTTT	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC/GA/JTAAATTTGGTCAATTCAGAACAATCCAAAT
WI-16905	75 C T	ACTTGGCCTGT GTGTTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTGTTGTTTATTGGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCA/C/JCCCACTGGCTAGAGAGTATAGACA
WI-16910	74 G A A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTCTTAAGGAGGTTATATCGCTATGACTTTTCATCTCAGAAAGAGTAAAGATGGCG CTAGAA/GA/GTATCTGTTATAGAAACGATACITCATTTTGGGCTGAACCCAGTGAAGGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATCTCTCTGCTACCCACAGACACTAAAATCTAGGAAATTTGAC TTTACTGCAGGCCATTAAACACCAGCAC/C/JGATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A C	GGAAAGCAGA CCTGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTCATGGAATAGGCTGGAGCACAGGATT TGGCTGAGGCTTCACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGG/C/CJCCA CGGGCAATCAGATGAGATG
WI-16947a	58 C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTCATGGAATAGGCTGGAG/C/GJACAGG ATTTGGCTGAGGCTTCACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGGCAATCAGATGAGATG
WI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTGTTTTACTTTAAATGCACACTACATAACAACCTAAT/C/JCTTAACTTGGTCCAACTATTT AGTATACTAATATGAGTTTTTACTGATAACTTGAATGCCATTAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATTT/CJACGGCTGG AAATCAACATGCCCTCTCTCTGTGAAGTTGTGAGCTGAGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60 T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAAAGTACACTGTGCGCCCTCATCTGAGAT/GJGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA
WI-16992a	46 G A TC	AAGCACCCAG AAGTACACTG	CACATTCCCTT ACAGTCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAAAGTACACTGTG/CJCCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA

WI-17010	23 T C	TTCACAGGA AAAGCCATG CA	AATAACGGT GTTTGAATGT CA	ATGTTTCACAGGAAAGCCATGTCATGACATTCAAAACACCGGTATTATTAGAAGCTCATTTAAT TGTTTAATGCAGACAAATAATCAAGGCTAACTAAAGCAGATCCAATGACCCAGTGATCAACCTAGA GGTCCACAG
EST17127 9b	74 C T	CACTCGGCAC TACACAGAGT	GGGAGGCGAGG GGTG	ATTCGGTCTCCAAACAGCATCCAGCGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGTCCTGGGAGCCATGGGGCACCCTGCCCTCCCCAGGCTTCTTAAGTAACAAT
WI-17040	94 T C A	AATTCCTTAT CATCTCAAGCC	GGACTATGGCT TATTCAGTGAT G	CACGGGTTCAATAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGACGATTC GAGAAATCTCTTATCATCTCAAGCCAGTCATCATCACTGAATAAGCCATAGTCCCAGTCTCGTTTTCC AATCTTCTCATATGT
WI-17044	47 G T G	GCCAAGGGAT TAACGTATAG	GGGATOCCT TGTTTAAGA	TTGTTTGTGTTTCTCTCTCTGCTGCCAAGGGATTAACTAGTGGGTTCTTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCCTGCAGAAATGGCAGGAATCGAAT CAAAAGAAAGCAAGTG
WI-17021	62 T A	TGGACTTGTC GCCTATACT	TGTAGAGTTAG TGGCAGCTGC	GCATGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTACGCCCTATAACTACTCTTAAG CAGCTGCCACTAACTCTACAGGCACAGTAACACTTTTACAGGAGCAGCATGCCAAAGTGCCTGG GAGTGCCCAATAAATCAA
WI-17065	90 T C CTT	CCAGAAAGGA AAAGCATAAA	CCCAAGAGAC AATGAAATCCT	TGTAATAAATGTAGACATGGGGGAAAAAATTCGTAAATCAACATGTGCTGTTTCTACTTCCGGTA CCAGAAAGGAAAGCATAAACTTTCJAGGATTTCATGTCTCTGGGT
WI-17066	32 A C T	TGTACAGCCA ACATCACTGTT	GAGATGTTGAA AATGTTCTGGA	TTATAAGGTTGTACAGCCAACATCACTGTTTCJATTCAGAACATTTTCAACATCTCAAAAAGA AACTGCAACCCATTAGCAGTCAATCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86 T G	---	---	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAAGCAT AACCTCCTACACAGGCCCTTTCJATACATAGGAGTATATTTGGCCCAAGACTCACCACTAGAAAGTATT
WI-17104b	108 T C	---	---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTCGAGCTTCCCATTCATCCCA AATCAGAAAGCAGTCAGTGGCCCCGTGGTTCCAGAGCGCTTTCJCTCTTTGTTAAGAAATTA
WI-17114a	37 T C	TTCCATCAAG GACTTTGTTT	TTGTATTATA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGAGTGTTCATCAAGGACTTGTGTTTCJGCTCTTCACTCTGCTATTATAATAC AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAGAAAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76 T G C T C T	GATGAAATTC AGATAGTCTTC	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCCCTCTTTCJCATATCTCCAGGATTCTGAGAAAGGCCCTCTTTGTCTGCTCTAATTT
WI-17163	43 A G TAACGTT	CATTCTTTGT AAAATAACAA	CAGAAATCTTGC TTTTGCCCT	GAAATCGAATACGTCCATTTCTTTGTAAAATAACAATAACGTTTCJGJAGGGCAAAAGCAAGATTCTG TAACCAACATTTGAAAGGGGACACAGGAGGGGCGAGGGGAAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAA



WI-17178	127 T C	GGACTCCCTCA	CCCTCAATTT	AGCAATGTCCCTCCCAATTTCAATAGCTATGATGGAGTTATCAGTTATCAGTTATTCAGAGGAAATTA
WI-17180b	81 C G	CTGAGGAGC	CAACTGCTTC	GGCGAGGGGGTTTAATATCTGATGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA
WI-17180a	47 T C	CACAAAATA	---	GCAGTTGAAATTGAGGG
WI-17180a	47 T C	TAGAGAATCC	TGGACGAGAC	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATCCTGCCAAGTCTCGTCGACAG
WI-17156	54 G C	TGCTCTAAA	CAAGAAATAT	GCCTTCAACAAATACCAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG
WI-17149b	79 T C	CTTTAGATATC	ATATTTGATTC	GGAGTC
WI-17149a	48 C G	CAAGGTTGA	CCACGACGTG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATTC/JCCCAAGTCTCGTCGCA
WI-17197	67 G A	GCAGAAGTAG	GGTGAGGTGGT	CAGGCTTCAACAAATACCAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG
WI-17198	38 A C	CTAGAGTT	ACTGAGAAAT	GGAGTC
EST18753	27 C T	CTACCCAGGCT	GGATCGCATGA	TGAGGTAGCAGGGCATTCCTAAGAAATGTTCTCTAACTTTAGATATCTCCCATTC/JCTCCACAGA
WI-17108b	74 C T	TCAAAGTAAA	ATCATATGCTC	ATCAATATATATTTCTTGTTGGAAATTTTAAATGTCTTAACTATCTGCCTACCATCCACCTCAAT
EST19067	41 A G	---	---	TAATATCTTG
EST19067	41 A G	---	---	CAGGCAGTTAATGTGCTGACATAGTAAAGGTTTGAAGGAGGAACTCTCATGACGACATCTCATGCGTGGAA
EST19067	40 A C	AAGGGTATAG	TGTACTTAATG	ACCCAAATTTGTCTATTCGTTATGAGTAAATTCGTTTAAAGAAATTTTCTCACA
EST19125	28 A G	---	---	CAGGCAGTTAATGTGCTGACATAGTAAAGGTTTGAAGGAGGAACTCTCATGACGACATCTCATGCGTGG
EST19125	28 A G	---	---	GAACCCCAATTTGTATGTATGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC
EST19125	28 A G	---	---	ATTTGCTATGTTGCCCTGGGTGGACTCCAGCAATCCCTCTGCCTCAGCAGAAAGTAGCTGGGCTAC/J
EST19125	28 A G	---	---	/A/GGTATGCACCACTCACCCCTGCTTATCAGTTTCGTTTAAAGAAATTTTCTCACA
EST19125	28 A G	---	---	TGATTTTCAGTACTTTTCTCCCTGCTGCTCAGTTTTCGTTTAAAGAAATTTTCTCACA
EST19125	28 A G	---	---	ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC
EST19125	28 A G	---	---	TTT
EST19125	28 A G	---	---	TCGCTATGCTACCCAGGCTGGTCTCATTC/JTCAGGCTCATGCGATCCCTCTGCCTCTGACGTGGCTGG
EST19125	28 A G	---	---	GATAAGACACAACCTGCCACAGGCTGCCCTAGGAGTAGTCTTAAATGCCTGATGGTGGG
EST19125	28 A G	---	---	TTATTTTAAACATAAACCAGATGCACCTGGTTTTCATTTTACATTTCTGTTGCCATTCAGTCTCAAAGT
EST19125	28 A G	---	---	AAACACATCT/JGGGAGCATATGATAAATCGTAGTTTAAAGAAAGCCATAGCACTTACAGAGT
EST19125	28 A G	---	---	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JG/JGTGGCATTAAAGTACATTCAACT
EST19125	28 A G	---	---	TTTTGAGCAACCCGCCATCACCATTTCATCTCCGTT
EST19125	28 A G	---	---	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JC/JAGTGGCATTAAAGTACATTCAACT
EST19125	28 A G	---	---	TTTTGAGCAACCCGCCATCACCATTTCATCTCCGTT
EST19125	28 A G	---	---	CTGTTTCTCAGAGATGACACTGCCAACA/JG/JTCACAGATTTGCATACAAATACAGTTATGTATTGGC
EST19125	28 A G	---	---	TATTCACAAATTTACAGTAGTGTCTTCTCTGAAAAA

EST20824 8	115 T G	AGTCGGAGT TGGACCGA	AAGATTTTATC TGGACCGA	GTGTGGAGCCGGAGTTTATTATTATTCAAATCAGTCTCTGTGAAACTCAGGGATTGAGGTTTTTA AGGATAACTTTGGTGAGTAGAGGGCCAGTAGTGGGAGTGCTGATTG/GJTCGGGTCCAAAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGCTA	TTGGTTAATGATGCCAGATGGGTGCATCCTCAGAACTTCTCAGCCTAG/GJTAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGATGAGTGGGACCA
EST21904 b	128 G A G G	TTATATGGCC ATTTTAATAA	GGCAGGTGTC AGAAAGCAT	TGATTGTGGGTCTGGGAGCAGGTGGGCAGTTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAATGTTACTAGGCTTTCATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTCTT	TGGAATAACA GCCCCAC	CAACAAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATTCTTTT/CJGTGGGGCTGTTTTCCAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCACCAAAATCCACAGGAGAAATCTTAAATGTTTACAAGCACCAATTTATCTGCT ATTCTGCCAT/CJACCGCATCTCTTCATGGTAGAGTATCACAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C ---	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATACATAAAAAATCCACCACGTAAACAG TAGCATTCATGGTTTTACTCTAT/CJGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G ---	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATACATAAAAAATCCACCACGTAAACAG CAGTAGCATTCATGGTTTTACTCTATTCGCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C GAGTTATAA	GGATTAGATC ATCTTTTATT	TGAATGCTAC TGTTTACAGTG	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAAT/CJACATAAAAAATCCACCACGTAAACAG CAGTAGCATTCATGGTTTTACTCTATTCGCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C ---	---	---	TCGAGGAGCTCTGAGGAGC[A/C]ACCAAGGGACGTGTGTCCTCCAGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTTCTCCCTTTACAAAACCTCCAGCCTCACCCACACAACACTGGCTGACAGGCCTTCT TAAGCCTTTTTTAAGTGT
EST22433 c	103 A G AA	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA	GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATCCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC[A/G]TCTGTCAGTTAAGCTGAAGCTGAAAT CTGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TATCTGCACA	AGTTTCAGTT GCATGAATTT	TATCCATTTCAAGAAAAAAAATGACTTAAAAATAACAATTTCTATCCAGAAAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T	ATCCTTTTGT C TCTACCCC	TTGCTGTAA TTTGACTGTAA TG	GCCTTTATGTCTCCTTTAACATCAAAATGTTTTATAACACACTTGATCCTTTTGTCTACCCCCA ATT/C/CATTACAGTCAAAATTACAGGCAATAATAATAGGTCTAACAGAAATGCTTGCAATTT TTATTTCTCAGCTTACCAATTTGTTGCTATCTCTGTACAAAGGTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTAAATCTTTGCCCTT/C/ATGGTTTTGACAGTTTGTGCTTTCT T
EST23021 0	108 T A	---	---	ACAGAAATTTAACATGCAAGTTTCATTTACATTAACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTTG
WI-17387	55 C G	CCTTTGCAGAT TGAAGAAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	TTTTTGGCTTGTCTGCAGATAGATGAAAAAGAGAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAGCTCCAGAGGCAG/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAAGC	AAAGGCTGTAGTTTGTGTTTTTCTT/C/GTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAGTCCAAAGGCTAGAGAAAGATATAGGCCCGAGAGAGGCTCAGAGATTTCTAGAGCGGCG TGAAGAATACCCACCTAAA
EST23733 9	31 T G TT	GGCTGTTAGTT TTGTTTTGTTT	TGCACCTTAAA TCCCATCAAT	CTGACACGTCCCTGTGTGGGGGTGCCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCGCCAGCCCT/AGTGGCCCTCGTCACTGGCCTTGGTCACTTTGTATTTCTGCTTGGTTGAAA TACCATCAGCCTTCC
WI-17470	83 A G CCAG	GTCCGTOCCG CCAG	CCAGTGACGAG GCGA	TTTTAACGAAATCTCACTACTGCAAAATGCATTTGTCTCTAGCTAAATGAATGCAT/C/JAGAGTATTG CCTGCAAAATAATAATTGAGATTTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCAATAG
WI-17519	55 T C A	GTGTCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TCCTTGATACAGGTAACCAAGTTTTGTAACTATTTCAGAACTTCACTGTATCTTCAAGTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GTATAATGTCAACATCAGGATTTCTTTTT
EST25356 3b	95 C G	---	---	TCCTTGATACAGGTAACCAAGTTTTGT/C/JACATTTATTCAGAACTTCACTGTATCTTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	GGGTGACGCTCCAGATGGGAGACAAGCCAAATTTGGAGAGAGATTGGATCCAGCTTCAATCAACATT ACTACCAAGTTATTTGATAATGATAGAACCCAA/C/JTAGGGCAATTTACATTTGACGCGTCATGC
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAATCAACATT ACTACCAAGTTATTTGATAAT/C/GATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGCGCT	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAATCAACATT ACTACCAAGTTATTTGATAAT/C/GATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCTTGTG TAAACACTCC	CAATCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAAGGCGCTACT TCCCTGTGTAAACACTCCC/AGJATATTGTCGATTCTAGCTATAAGAAATGGGGCCACTAAGTGGGCTC

WI-17623	46 T C ...	---	---	TG TGG TTTTAA TTTTCCATATAATTAATGTTGGGCACATTTCGCAATGCTTACTGGGTC ATTCATATATCTTTGTGAAGCATCTGCTCCAATCTTTGCCTGACTTTGGAGTTTTTGGT
EST26419 1b	46 T C ...	---	---	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGATTCGAGGAGTCCAAACTTCT TGGAGGAAAGTAATTCATGTTAAATGTCATGATGGCTGTTGAGGAGAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	35 C A AG	CAAGAAGTTTG GACTGCCC	---	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGC(A)AACAATCTGATGGCAGTCCAAACTTCT TGGAGGAAAGTAATTCATGTTAAATGTCATGATGGCTGGTTCGAGGAGAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780 5	69 G C ...	---	---	TCAGCTTTAATTTAAGGACATGTAATAAAGATGCAATTTGACAGGACAGCAGACTAGTTCAAGC AG(G)C)AGGTTAGACCAGTAACAACAACCAAGAAAGCAAAAGTCTGTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ...	---	---	TACTTCAGTTTAAGGCAAAATTCACACAGAGACTGTCTC(A)G)GAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCATGTCATGACGGGGAAGCAGAG
EST27152 1	101 C T ...	---	---	CAAAGGATTTTATTTTGTCCCTAAAGTAATAATCTAGAAAATAGCAACCCACTGCAAGAAAGATT CTATACTAAACATTTTCAATCATCTCTCTCTC(T)CTCAGATGGTGTACTCTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 0a	33 G A ATTT	GCTGTTGTGAT GCTACTGTAAT G	---	TTTTGACACTTTGCAACAATTAATAATTATC(G)A)CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTCTGTTACACATTCGTTTAAACAAGAACCCATACATT GGTAAATTCATCTCT
EST27662 4	51 C T CTCCAGTCTTG C	TTATGGAATG GCTTATGTAAC	---	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTCCTGTTCCAGTCTTGCTTAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACTCTTGTTAGGAATGTTT
EST27788 3	100 A G ...	---	---	ATTTTATTAGCGGTACAATTCGAAGGTGTAAGGGTGAAGGAAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAACTTTACATTCAAGGAC(A)G)GCTTCCAGACAAGCCATGTAGAACCCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAATTC	GTGCAAGAGAGG TACTCCAAGTA C	---	TCCTCTAAAACCTTCTCTGTTGGATCCCAAGTACGTTGGAAGTATCAGAACCCCACTG(A)GTACTT GGAGTACCTCTCTGCACCAAGATAGTGGCTGATTTCTGCTCAGTCACAAATTTTACTTGAA
WI-18369	58 G A ACATC	TCAAGAAGGCC TTATCCATTT	---	TAAAAATTTGAGATACATTTCCCAATGTAACAATAAATTTCAATCTGTACACAATC(G)A)AAATG GATAAGGCCCTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ...	---	---	TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTA(T)C)AAAAAGATGATCAATCCTGTTGCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACCACCGCGTCTGAAGGAGAGACTGCTGTTGTG TCCACCTCTTATTCATAG

EST28483 7	31	T A	GGAGTAAAG GTGTTCTTCT TTAA	TTTCTGCAAT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTTCTTCTTTAAAT/AJATGGTATAAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACAACAGAGAACATGAGTTGTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50	T C	TGGGCTTCC TGTC	TGGTTGGCAG TGTC	AGAAITGGTCTAGTATCGTTACAGATTCGGGTGATGGGCTCCCTGCTGCT/CJGGACACTGCCAACCC CACAGCTGGAGGGGACCTTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68	T C	---	---	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGTCTATTAGTTACATCATACCAAGTGTACATACCTG TT/CJACATGATTTATGGCTGTGATGTTGACCTCAATAACCTGGCTGATGTATGTGCA
WI-17730a	39	A C	GACCACAGAA GTGAAGTGT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGTCTATT/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTGATGTTGACCTCAATAACCTGGCTGATGTATGTGCA
EST29041 5b	53	G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACATTAAGCATCATTTGTCACT/GA/GCTAACTCCT CAAATCAACAATACCCCTTTATTTAGCCATGAAAAAC
EST29128 4	58	A G	---	---	CTTTAGAGGACACCAGTCTGTTGGACTTAGGGCTACCCCTATTCAGCAGGTGCCA/GJTTATTT TCACITGGTACGTCGTAAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103	C T	TCTGCCAGCTT ACAGGCT	GCGTAAAGTGC TCATTCTCTG T	ATTATTAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGATACCTGCAACAGACACAAA AGCAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/CJACAGAAAGATGAGACACTTACGCGATG GCCATGATACACAGCAGTGA
EST29936 8	121	G C	---	---	TATTTGATGCTTAGGGAAGATTCTGATTAGAGATATTAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA/GCJAGCTCAGTA TCTGGAATCATGCTTCTCTG
EST30223 2	99	A G	---	---	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTTAAATATCC/A/GJGGATTTAATTTCTCCTAGTTCAATCTTGGGA GG
WI-16260b	86	G A	---	---	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCAGAA GTTTCAAAATATAGGTAGTGC/GA/JATAACACAGGCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59	G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCAGAA AGAGTTTCAAAATATAGGTAGTGCATAACAGGTTCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30	G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTCTG/GA/JGCTGTTTCTTATACCCCAATATCATAGAAT GTTGTGCTTCTATATGTTTCAGCTTCAAAATCTTTTGTGTTAATCAATCCAAATGAATTACCTGAAT TTCTCCTCTTGTTCAAAA

EST31951 4	87 C T	GGGTTGTCCAG CCAACA	CCCACCAAAAT CACCTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGTTGTCCAGCAACA[C/T]GGAGGTGATTTTGGTGGGAATTCCTTATCACAATTTCT
EST31968 8b	95 T G	...	...	CGAATTTGCTCTCTTATTTTGTGATCTAGTAATCTAAAGATTGGGGGGGGTGTACTATAAGT GCATTTTATAATGGGGATTTCTGCTT/GA/AACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75 T C	GCGGGTTACTA TAAGTGCATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGCTCTCTTATTTTGTGATCTAGTAATCTAAAGATTGGGGGGGGTGTACTATAAGT GCATTTT/GA/ATAATGGGATTTTCTGCTTAAGTCCCACTGATTCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCCC
EST32063 2	103 C T	...	...	TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTCCCTCCGACCAGATGTGCTGGCCAGAGC TGGCTTCCCCCTCCAGACCTAGCTGGCTTTGTAGT[C/T]GTTCCAGGCCCATTTGAATAGCAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G	...	...	AAGGCTTTCCAAAGCATTCAAAGGCACCTGGGTGTGGCTCTAAGTTTCTGGTCACTGCAGCCCCA/G TCTGTATTAGGGAGCACCCCAAGCCCAAGTAACAATATGGTTCTTGCAG
WI-17800	29 C G	GAGAACTCA TT	TTTCCACAT TAATCCCAGTC	TGGACATGGGAGCACAGAGAACTCACT[C/G]AAGACTGGGATTAATTGTAGGAATATTTACACAG TTTCCACAAGTCAGAGAGCTAATCCCAACCCCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGGAATACCC
WI-17857	34 T G C	CCATAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG	AAACTGTCAATTCCTAAAGTCTGGGATGACTTTCCTT[G/A]TTCTACATCAAGTAGAACCTAAGCCAAAT TCAGAATCAGAAATCCTTTTGTCCATCAAAATCCAGCTAACTCCAAAGCTGAATTAATTTTCAATCT
WI-17860	121 T A	TTTCCAGCAA AGCAAATA	ACTAAGGAGG AGTCAGTCGG	GTAICTGATGTAGTTAACCATGGCCCTGTCATGATTATATTGCTATAAGGAAGGGGAACAAATCTTTA TAGTGCCAAAGATAAATTAATCTTGGTTTAAATCTTTGCCAGCAAAAGCAAAATATTA/CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43 A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAAATGTTTATTTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAAAGTACCA
EST33301 4c	80 G A	...	...	GAAAAAAAGTCAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACAAAGCATGATC AATGCCACGAGA[G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	63 G A	...	...	GAAAAAAAGTCAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACAAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44 G A C A	AGCGTGGTTTT CAATACTAAA	CTGTATTATT GTTAAATATT	CTATCCAAAGATATTTATTGCAGCGTGGTTTCAATACTAAACA[G/A]TGTAAACAATGCAATATT TAACAATAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAACTACTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC OG	CAAGTGAATATTGATACATGGCTGACAMGACATGACAATAAAATGAACACACAGTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCGGTAAMATGCAGTTAAACAAACACACAAAATGA
EST34149 5	69 A G	TGCCAAATAC TCAAGTGTGA GAT	AACTACTAGCG AGAACAATA ATAAAATC	GTITTTCTTTGAGTGACACAAGCTTGTTCAITTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TJAGIGATTTTATTAGTTGTCTCGCTAGTAGTTTGGTATTCATGMAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	GGACCATATG ATATATAACT CCTAAAGC	---	TGGGAAACACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAACACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC/AJTACAAAGATTAAAGAAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAAATTTAATGGAAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCTAAAGC/CJTJGGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTCATCA
WI-17993	118 A C	GTAGAGGCGA AGGAAACAG G	AGGCACATGGG CAGC	CTCAGTAACCTCCGGTGATAATCTGCCATTTATTGATTTATTATGATAAAACAACTCTCATTTGTA AAAAACAGCTAAGGTGACATCTCCAGACCCCAACCACTGTCCCTGTAATGTA/CJCTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84 A G	GTAGAGGCGA AGGAAACAG G	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGAAGAGCATGAAACAACATCTCCCAGGCCCTCGCAGT AGAGCGAAGGGAACAGAG/GJCTGCCCATGTGCCCTGTCTCTAAAGAGCCACCCCTCAGGTTGATGT CACTGTGGGAGACCGGGT
WI-17136	33 C G	GTAGAGGCGA AGGAAACAG G	AGGCACATGGG CAGC	ATTCCTTTATAAAACACCATGTCCCTAAATGT/CJGJATTAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGCCCT
WI-18041	24 A C	GTAGAGGCGA AGGAAACAG G	AGGCACATGGG CAGC	GCCACTGMAAAAAGGTGCTCTCC/CJGJTTCTTAACCTCCCTGGACTCCCTCATTGGAACGAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57 A G	CACAGCCCTGC TCATGTACGA ATC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCC/CJGJCTTGA GATTCAGAAATCCAGAGGGTGTCTAGTCTCTGTTAGGTGCTTCTGTGACATTTCTCTTTG
WI-18052b	67 A G	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGMAAATGCTACATAGGCTCCCTGAGTCTTTCATGTACGAATCT/CJGJTTACACATCTT A/GJACAGCAGAGCTGCTGAGGGAGGGTGTGTTTAAATGCTGATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C	GGGAGTGGGG GAGTAAAA	CGTCAACCTGC TTCCA	AGCGAATGMAAATGCTACATAGGCTCCCTGAGTCTTTCATGTACGAATCT/CJGJTTACACATCTT AGAACAGCAGAGCTGCTGAGGGAGGGTGTGTTTAAATGCTGATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A	GGGAGTGGGG GAGTAAAA	CGTCAACCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAA/GJATGGAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTGCTCAGGTTTGTAGCAACAGAGGTAATG

WI-18064	54	GA	AGTGTATG AGCTGATTTTC C	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCAAAACCCTGTGGGTAGCTGCTAAGCTGTATTTTCAGAG/GA/GAATGTAC AATCATACCACCTGGGAGAAAGAGTAAGCACAGTCTTATAGGTGCCAAACTGGGTACCTGGGAG GCAGAA
EST35347 2	97	TCA	GCATAAAATT TTCCAGTTGGT TCA	CCCTCGGCACC TGCT	TTAGCACCAATCTTAGTGGAGCAGGATCTTGATCATGGGGTGAATTTTGTATCTGGGCTTCAT GGGATGCATAAAATTTTCCAGTTGGTAAGT/CJAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	AC	AACCCACTAC TTACTCAGAGT GTGTAT	AAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT/CJATATTTAACACATGAAAGATATAATCTTAGAAAA ACCTCCAGTTCTTATTAGTTTGTATTTTCTGTACTCAGAAAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80	CT	---	---	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTTTTGTAAATTTAAATCTACTATGCCGTG TTTGACTTTTATCTTCTTATGTAAATGAAGCCAAATGCAITGTTAATCTCTCTCTTGGGTGTAT
WI-18080b	65	GA	---	---	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTTTTGTAAATTTAAATCTACTATGCC/G/ ATGTTTGACTTTTATCTTCTTATGTAAATGAAGCCAAATGCAITGTTAATCTCTCTCTTGGGTGTAT
WI-18080a	41	T	GCAATATCA ATATCAAAT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCT/CJTTGTAAATTTAAATCTACTATGC CGTGTGACTTTTATCTCTTATGTAAATGAAGCCAAATGCAITGTTAATCTCTCTCTTGGGTGTAT
WI-18086	63	GA	---	---	GTGGCATCCTATAAAAGCAGCCATGTGTTGAACAAATGATATGCACAGAAAGCATCTTCT/GA/ TGGCTTTGTACACGGTTTCTTCAAGAGGAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18115b	71	CT	---	---	AACTACATAGTATGGTGCCCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGTACCTTTGGTATTCCT TTC/CJTTTGGTATGAAGACAGACCTCTGCTGGAGGACTCATTAACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115a	70	CT	TTAGTGTACCT TTGGTATTOCC A	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGTACCTTTGGTATTCCT TTC/CJTTTGGTATGAAGACAGACCTCTGCTGGAGGACTCATTAACAATGTAAGAAAGGGGTGAG TCAGT
WI-18136	78	AG	---	---	TTTGTAGAAGCAGCTCTGTAAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTCTCTTTA GGTAAATTGCA/GJTAAGAACAATAAAGCATTTTAAAGTCCACTGCCGCCCTTAGAAACT
WI-18169	115	AG	CCATCTTCCG	GAGTTCTGCTT	GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAGCAGCCATCTTCCGGAAGCTC/GJTTGGAGCACAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18190b	26	GA	---	---	TGAAAGAAGTCGACACAGCGGACACT/GA/JTCATAAGTGGAAACAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGATGAGCTGGAGACATTAATCTCTGGCGA



WI-18190	62 G A	...	AAATATATAC AACACTCCCTT	CGTTTACCAT TTGTTAAGCTT	TTG	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGGAAACAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAACTCCTGGCGA GACAGTGAACAACATTGAAACACAAATACAAACAAACATTAGGAACAAGAAATGTGTAAATCCAA TGTGTGAAAATATATACAACTCCCTCAGATC[A/C]CAAAAAGCTTAACAAATGGTAAACGTA TGTGTTCTTGAAC ATTGATACAGCAATTCCTGAGTACAACTAGGGGACAGGTATTTTACAAAAAATAGAGCAGA GTTCTGCCCTG[A/G]GTGCGGGGGGAGAGAGGGGATTCAGCAATTTGGTGAGTATGTAAAT CCCTCAAGTTAATTCCTTC CATTTCCGAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/G]AA CCCCGAAAACCTTTATTTTGAATGAAGTTTTCGCTCAGAACTGGGCAGAACTTTTCACATTCTG AC
WI-18181	100 A C	CAGATC	AGCAGAGTTC CTGCCCTC	AAATAAAGGT TTTCAGGGGT	CTTCC	TTTAAATGCTTAGATTTTCTCAGTATTTTATCAANTAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGCATTTCCGGCAGAAAGTGGC AATATCCCAATGTTATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAA GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18215	78 G A	CTGCCCTC	AGCAGAGTTC CTGCCCTC	AAATAAAGGT TTTCAGGGGT	CTTCC	TTTAAATGCTTAGATTTTCTCAGTATTTTATCAANTAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGCATTTCCGGCAGAAAGTGGC AATATCCCAATGTTATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAA GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18232	60 T A	AA	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGT	C	TTTAAATGCTTAGATTTTCTCAGTATTTTATCAANTAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGCATTTCCGGCAGAAAGTGGC AATATCCCAATGTTATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAA GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266c	119 C T	...	AAATAGGAAA TATGGACTATC	TTTATGCAATCA TTTGTGCA	...	TTTAAATGCTTAGATTTTCTCAGTATTTTATCAANTAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGCATTTCCGGCAGAAAGTGGC AATATCCCAATGTTATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAA GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	...	AAATAGGAAA TATGGACTATC	TTTATGCAATCA TTTGTGCA	...	TTTAAATGCTTAGATTTTCTCAGTATTTTATCAANTAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGCATTTCCGGCAGAAAGTGGC AATATCCCAATGTTATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAA GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	TTCAAA	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGT	C	TTTAAATGCTTAGATTTTCTCAGTATTTTATCAANTAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGCATTTCCGGCAGAAAGTGGC AATATCCCAATGTTATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAA GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G	AA	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGT	C	TTTAAATGCTTAGATTTTCTCAGTATTTTATCAANTAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGCATTTCCGGCAGAAAGTGGC AATATCCCAATGTTATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAA GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18330b	66 A G	...	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGT	C	TTTAAATGCTTAGATTTTCTCAGTATTTTATCAANTAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGCATTTCCGGCAGAAAGTGGC AATATCCCAATGTTATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAA GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT

WI-18330a	49	GA	AAGA	TCCTGTAAGA AATCAGGGAT	AGTCCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAAATTTTTTTTGTGAT TCACA
EST37564 5	85	T	CAGA	AAATCAAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACGTCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATT[C/T]CTCATTGAGGCTCCATAGGCTGCAAAACACATCAAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	GA	TT	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACAACAAGTAAGGAGACAGCTGGGCAGTTCCCAAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGGGAGGCAGA GT
EST37624 6b	102	GA	---	---	---	GTGGAAAGCAGCAGCTAAACACACACTCAATTTGCATGAATCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	CT	---	---	---	GTGGCAAGAGCAGCTAAACACACACTCAATTTGCATGAATCCAAATACGAACAGTGCACGCTGATGG TGCGCTGCAGTCCTCTGCCGTGCTTGGCTCTCTGGACGGTTCAATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	CG	GCATCA	CCAGCCCTTA GCATCA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTACCGTGCAGGTGGCCATGAAGCCCAAGCCCATTCAGACATTTTCAGA TAATCCAGCCCTTAGCATCA[C/G]TCATCTTCAGCTTTGAGTCCTTCCAGCCAGGTCCAAGCTT GTGACACAGAGACAAGCC
WI-18012g	117	A	G---	---	---	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTT[C/G/A]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012h	113	GA	---	---	---	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTT[C/G/A]GTGAAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	CT	CCCTT	GCCACTTTTC CCCTT	TCAGCGTGTAT CAGGAACA	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTT[C/G/A]GTGAAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T	C---	---	---	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCAGACTTGGAAAG AGATCCCCTGCTGCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTGTGAAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A/G	CTGCAATTG	GCAAAAAGGA CTGATTAATAA	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCACAGAT/ATTTCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTG[G/A]G/ATTAAGTTTATTAATCAGCTGACITTAGCATTTGGGAGATTATCTGGAT

EST38512 7	91 T G	TGACGATGGC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAACTGACCCAAATTGGTAAACTGTGCTGGACTGAGAGAAACAATGAAAAATCTGTAAT ACCTGATGACGATGCCAATCTTCGTTGTCCTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACTCC TAAAGATCT	TCTGTTAGGAC TTGGGGA	CCTGACCTCCTAAAGATCTTTTC/TJCCCAAGTCTACAGAAATGGTATATCTCTCGGAAAA AGATGAACGTCAATGATGTGCTGCTCTGCTTTTACAGCTTTGATTTTTTGCTTGAGAACCTTG TCCTCCCTGCTGATTT
EST38575 1		GAACATCCCA TGTTCTGTTT	AGGGAAGGTA GTATAACACAT	AGTGGTCAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA T/CJCTCTTATGTGTTATATACTACCTTCCCTTCTCTTCTTATACACATAGATTTTCCTTAATTGCAGC CCA
EST38616 9	66 T C A A	CCTGCTCCGOC CTTC	AAGAGA GAGGAATGGAT GGTGGC	CCATCTAGGCAGGCTACCTGAGCTCTCTGTCTCCAGAGTGGTGGTCAAGCCCGGGGGGCGCTGG AGTCTCCGGGGGGGGGGGGCTGCTCCGGCCCTTCJGJGCCAACATCCATTCCTCCAGGGG
EST38652 8		TCTGAACCTGGG CATTTCAA	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTCTCTGCTGCAGCAGGAATATTACAGTCTGAAGTGGGCATTTCA/TJCJGCGTG GTAATTTTCTCTTCTTCAATTTTGCAAGTAAAAAATCAT
EST38654 5	59 T C	AATGGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAAATGGTCATTTTAAATATATCAGTTTTACATA/TJCJAGATAGAAGATTAAAGACCAT CACTGAGTCAATAGCTCAGAGGCAGAGTTAAGATTGGACCCAGGAGGTTGGTTCCAGCATATA GGATCCTCACTCACCTGGGACAGCCTGAGAAAGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTCCCGJAGJAGGCCAGCGGATGTGTGCCCTCTCTCCCACTCATCTTTCAGGAACACGAGG ATCTTCTCTCTGGAAA
EST38707 9	75 A G ...		...	TGAOCTGTATTCTTCACTAGAGGGGAGAAATCACTACCTTCTTGGATGCCCTCCACTCTACTTGT CTCCCTGAGGTGATATGGJAGJCCCTTAAGTCCACGATGGTGACCTAACTCAGTTTAAATTTCTTGCC TAGCAGCACC
EST38759 2	86 A G	TGCTCCCTGA GGTGATATGG	TCACATCGTG GACTTAAGG	GACTCTCAACCAAGAGAAATCAATAGGAGAGGATTGGCT/AJTJTTGAATTCAGAGCAAGCCCT CTTACTGAGAGGTGAGCCCAAGCCCTCCAAATGCCCTTTCATGAGTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	
EST38815 4		TGTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTTATGTGTGTTCAACAAG TGTTATGAGAACCCATTACACA/CJA/AAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	91 C A C A	CACGAGTAAA AAGAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTCTCCCAAGTTTGGGGTGTTCATATGTTATTGTTATTGTTATTA TTCAACACGAGTAAAAAGAACTCATGAC/CJTJCTCCTTGGACTCGCTCCTCTCCCCAATCTCGAT ACCGACTGCACGTGTG
EST38865 2	98 C T	GCCTGAGAAAT TGAC	GGAAGGACGG AGGACACAG	CCTTAATGGATTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTG ATGCT/CJCTGTGCTCCTCCGCTCTTCCCCAAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGCTCTAGTTGTTAA

EST38878 9	47 T C	AACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCT CA	CCATGAGAACCAAGTAATTAACATCACTACTAGCCTAGATCCTAAATTCJTGAGGACATGAGATTT ATTGAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTTCCC TTATCAATGTCTCATCTCACACATCTTTATTTTATTTTATTTTACCTTTCTCAAAATATCGGATTGTTGC TCATGAGAAATAATGGCTGAGGGAGCTGGCAGCGAGTCTCTCAJGCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 GC	...	...	TTATCAATGTCTCATCTCACACATCTTTATTTTATTTTATTTTATTTTACCTTTCTCAAAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCAGCGAGTCTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TTT	CAA	TA
EST38909 5	47 A G	GCTAAACG	T	GCACTAAACTAATCACTTTCACTTTGGAATTCACACAGCATGGCTAAACGJAGJTAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATCTGCTGGAGGGAATATAAATTT
EST38911 9	85 A G	CAC	GAACAAAGCG	AACTGAATGGCAGTGAACAACTACACATCAAACTTAGGAAATGTGTTAGTGTGGTACGTTGAG GGAACTTATAACCTCACJAGJCGCTTTGTTTCAAAACACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C	GGTGGG	CACTGCAATCT CAOXXX	TAAACATCCCATTAATCCCTTGGTGGGJGJGGGGGGGGTGGATTGTCAGTGTCTCAAGATAAA TATCACAATATATCAAAACTTCAAAATTTGCTATGCTATGCATTACACACTGACATGAGCCACAAACATTT CCTTTCACAGGGAGCTGAC
EST39002 0	42 G A	TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCTGGCAGATCCCGACCTTCGGTGACCGJAGJAGGCTCCCTGCCAGGGCTGG CCCCTGACCGGGCTCCOCAGCTCGGCCCTGACTGTGGAGGAGCTGAAATAGCTGACATCCGCAACCT C
EST39004 8	79 T G	CCTAAGGAAT	ATCTCGGCTGG OQGC	CACGTGGCCCCAAGTTCCGGGTCTTCCCTCAGTCTGGATGGCTGTGGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTTJAGGGGCGAGGGGGCGATGCCGCCAGAGATGGTCTGTAGCCCTGTGGGTC AAGACCTAACTTCTGGA
WI-16398	90 T C	TCA	TTGATAT	AAAGATAATGTCTATCACAAACGCAACATATAGAAACATAAAGAAATAAGTATCCACCCCTAAAT CCCATTATTCATGATATTTTCAJTGJAGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C	ACT	AAAG	GGTGTCTTTCATGATTTTCTCATTTCTCTATCAGGTTTCTGGTCTTGTCTCTCAATTTTAACTT T/CJCTTTTATATAGGGAATAGCCCTTAACTGTGGTACATGCTGCCAAAATTTCTCTCCAGTT
WI-16406	24 C T	AGG	AA	GCITTAATGGCTACAGAAAGAGGJGJGGTTTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTATATTATGCAATTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCCTTTTATTCATGATTGTTTCATCTGAGAAATAACCTCCTGCTCTAATTTCCAA(C/G)ACTATGTT TAATGATGACTCAGTACCTATAATGAGACTGGAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAACAG GGATGCC	GCACAAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC(G/T) TTCTCGGTACTATGTTTAAATTGCTGCTGAGCCAGCAACCTCGAGTTACCGGCCCTTTACCCACAGCC AGCTCTGCTGCTGCAT
EST39366 2	72 T C	---	---	AGAAACATTTCTGCTGATCAGAGGAAGATGTATGTAGAAAATCAGAAATCTGACTGAATTCCTAAA ATCTAT(C)ACACTGAGAGGAAAATGGAAGAAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCTAGA
EST39371 9	86 A G	CATTGGATT GGTGAGAGG	TGATTTGAGAC ATTTCACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAAGTTTATTTATGTGTGTAATTTCCAGTTGAGCAATTTTTCAT TTGGATTAGCGTGAGAGG(A/G)AAAAATGTGAAATGCTCAAAATCAATGCTTCTTCTAAAAGATT GACATTGCCAACCTGCTC
WI-17177	23 A G	---	---	ACAAAGTGACATATCCAAACCACCIAGTCCATCCCCACCTGTGCCCTATTCTTCTTGTTCTTT AGAGCCCTTTTTCAGCTATTTCTGTGTAAGCAAACTGCACGAAGGCCCTCCCCGTACTCTCCCCCTGGAA G
EST39428 8	31 C T	GCTCCACACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGTTCTCTGGTTGCTCCCAATTTTGATT(C/T)GGTGGCTTCATAAGGGACCCAGGATTTCTGCATT TTCTGGGTGGGCTTAGGTAATTTCTGTGGCTTTGGTCCACAGACACAATTAAGAAGATCAGGTCT GGCTGTGCTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGGTCCGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT(C)C/AATAACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACATTCA	TCCTGGAAAAAC TGACATAAAACC	AAAGCCCTGTAACTGAAGCTAGACAACGTCACACTTTTGGAAAGAAAATAACAGGAACCTATTATAT ACGTAATCACATTTTATACCTGCTTACTGACATAGGACTTCAGAGTAAT(C/T)GGTTTATGTCAGT TTTCCAGGATTTCTCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACCTGAACAGAA TGCAGGAGGGTGG(C)AGAGAGGGGCCGAGATTGGGTGTTTTCAGGGCAGAGAGGTGAAGACCCAG
EST39501 0	81 A G	AAAGATTCCCT GTAGACATCT	CAC TTGCAATT CTGAAGGCT	TGCTTACAAOCCATAACCATAGGCCATGTGTTTCAGACATTTTGACCAAGCCCTAAAGATTTCTGTAG ACATCTAACATTAG(A/G)TAGCCTTCAGAAATTCAGAGTGAAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C	---	---	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CAIGCTTTAGCCATAC(C)C/ATGGTAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAAATGGGACTGCTGAAGAGTGACAGTTGGACCTTACTTTGGTGACCCCATACAGTTTGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGCTTGTGAAAGTGTAAATGTGGCATG GCTATGTAGACATAAAGA
EST40601 9	78 A G	GCGTGAACCT GAAACAC	TTCTTGAAGA AAGGCGTC	TCCAGGATGGTTTATTCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGTGACTCGCGTGGA ACCTGAACACAGAGGACGCTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTTCAGGAT	GCACACCCCTC ACACTGTTA	TCCATTGAGTGATCACATCTTCAGGATAGGTAGTAAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGGG TCA	AAACTGATTT GTTAAACATG CTAC	ATGTCATTCTGGTCTTTATTTTGGACA(C/T)GTAGCATGTTTAAACAAATCAGTTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATATTTTTCACAAATTTCTCATCAGCTGTAAATTCA
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC C	AAATCTCAGC ATTGCTATAAG C	AGAGAGACAAACAGAAAGATAAGGGAAATGGGAAACAGAGTGAATTAAGCAAAATCTTGGA TTCAGATTCCATTAAACAGGAAGTTTCTCNAAAAAATCAAA(T/C)GCTTATAGCAATGCTGAGAA TTTCATAGGTAAGTCTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTGC TTTAAATTTAC TC	AGAGAGACAAACAGAAAGATAAGGGAAATGGGAAAG(C/T)JAGAGTGAATTAAGCAAAATCTT GGATTGAGATTCATTAAACAGGAAGTTTCTCAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTAAGTCTCATGGGA
WI-18425b	101 T C	CACCTGTCT AGACAGATTTC	---	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC CTAGACAGATTCA(C/T)GCACACAAACAGAGGTTGGGGTACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81 A C	AGACAGATTTC	CCTCCTGTTGT TGTGTGCA	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC CTAGACAGATTCA(C/T)GCACACAAACAGAGGTTGGGGTACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18449	129 C T	CTTTTGGCTCT AAGTGGGACT	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGMACTATAAAAGGAAAGGAAAGAGAAAGTAATCAAGGGAGGCCAAAGTG GGAAAGCTGATTGCTGATCTAACGTGTTCCAGTTCCTCTTTGGCTCTAAGTGGGACTA(C/T)TC TGGATACAGTCAGGGGAG
WI-18457	120 T C	---	---	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGTGGCCCCCAAGACATTATTTTATCTT AAATGTCCAATATCTGCCTGATGCTGTGTTGTGCACATTGGGGCCACAGT(C)AAATAGGCTAAA AGGCAGTCCCACCTGCT
WI-18462	39 A G	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTTCT	GGTGTATAGCTGCTGTACACCACAAATGGCAGAGGTGA(N/G)TAGAAACCATCTCAAGCCATAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG
WI-18476	60 C T	GGTGGGGTGC GAGG	GCACGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCCAGAGGGTGGGGCCGGGCTGAGGGTGGGGTGGCGAGG(C/T)GGT CACTCCCATCGTGGCCCTGGCGCTCCCTCCACTCACCCACAACTGGCCAGTCCACAGTTGAGGT

WI-18491	109	G A A A A T G G T	A A C A A T G G T	CGTGTGCATT	CTAATGAGATGAATACATGAAGGGCTT	AGCAGTGCCTAAACACAGTAAGTAACCAACAAT
EST50757	79	C T C T C T C T	G A G C T G A G G	ACCTTCACCC	GGTAGGTGGTATTAACTATTATTAAATCCAGATGAC	[G/A]GGATTACAAGAAATGCACA
WI-17675	103	T C A T G G T G A C T T	G G A C A T T T G G	GGGGAACCAAC	AGCCCTCCACTCTGCTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTCTCTTTTATAT	OGT
WI-16543	67	G T T C G	C A T T T G G G T T	GATTTCATCATT	GTGAGGGCCCTGGGCGGGTGAAGGTCAGAGA	
WI-17687	107	C G T T G G G A A	G C C A A A A G G	TTACTTTTGT A	GATCTTGGAAAGCACTAGAACTAAACATCTTCACCAGGTGCTGAAGAAAGTGTCTCGTTTTAAT	
WI-17690b	79	A G ...	A G C A T T T T T C	GGCTCTGCAATC	TGCCAAGCAGGGATGTGGACATTTGGATGGTGACTTTTCCCTGGGTGCTCCCATAGATTCAACAT	
WI-17690a	63	G A T A G C T G T G T T	G G T C C T G A A T C	TTTGTAAAGCTGAAGTT	TGCCTCTAATGGTGCTA	
EST51717	128	C T T G T G A G C T G T T	G C G G A A G A C A	TTGAGGCAATA	GATCCATTACCTAGGGTAAATTTCTCTTACTACACAGTGGAGGCAATTTTCTAGCTGTGTGATT	
EST51717	39	C T ...	T G G T C A C T T T G	GGCTCTGCAATC	ATCTGAGATGGAAGAGTTCATCCAAACCATCTCCCTGACCCCTGATCCCATGGAATAATGTGTC	
EST53012	97	C T G G G C	T G G T C A C T T T G	GGCTCTGCAATC	TTCCACAAACCGGTCCCTGGTGCCAAAGGTTGGGAA[C/G]TGCTGGTACGATGGAATAAT	
EST53349	96	A G T A C	A G T C A C A A T G	TTT	ACAACATGTGAAGAAGATATGTGCTTACTACACAGTGGAGGCAATTTTCTAGCTGTGTGATT	
EST53389	74	A G C A	A G A A C T T A A A	CAATAAATGCT	GGCTCTGCAATC	
					TTCCAGGTTGACAGGTTTATCCACCCCTTCCATCCCATGGCCACCCAGGAGGAGACAG	
					GTGCTGGAGTGTGGTCACTTTGGGGCC[C/T]GGGTGGGACAGGCCACTGGGTTACATTTCTCTGT	
					GGCAGGTTGGGACAC	
					AACTGCAATAACAAACAAACAGAAAGTCCAAAGGCTAAAGCTAAGCTAATTAACACATG	
					AAGTATATGTTGAAGCAGTCACAATGTAC[A/G]AAATGTGACAAGATATCCAGATGTTTAA	
					TTTCGAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT	
					TAAACAC[A/G]GAGCATTTATTGTAGAAAGGGCAAGCTTACACTCAATAGGTTTTAACATGAAC	
					ACATTAAGGGGAGATGGCC	





[illegible]

TGR- A003P30	117 C G ---	---	ACAAAGTTCAAAGGAGAACTTCTTTGTTTAAATGCAGCTGTGCTCAGAAGCCTGTGATTTCTCTAGGA AACCATCTGGGTTTAGCCCATTTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TGR- A004S34	156 C T A	TTAAA	GCTTGCTTTTATGTTAGTTCGGGGGAAAGGAGGGGCTGACAACCCGACAGCATCTGGACACCAGC AAGGTCAGGGGAGTTTGAGAACTCTTTGCTCTGGCTAACAGTCTGTCATGTGACATAGCCA AACCTCTCATTTCTTATAAA[C/T]CTTTACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TGR- A004T44b	97 A C ---	---	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT[C/A]AAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAACAATATGACTTAGCAAGAACAATATAG
TGR- A004T44a	69 G A TGA	GGAAGATAAA GCGATGCAAAA TTCTTTATCA	AACAACAGTGTAAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGAT TGA[G/A]TATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAACAATATGACTTAGCAAGAACAATATAG
TGR- A004V08	60 T C GGCATTCTCT	TCCTCCACCA AAAGGC	CCTACAATCCTATAATTTGCAAGGGTTGGGAAGGATGCAGGAAAACAGGCATTCCTCTA[T/C]GCC TTTTGTGGGAGGATCAATTTGGTGCATGCACCTTAGGGGACAATTTGGGCAGTAGCTGTCAAATTTG AGTAGCTGCAAAATTTCAAA
TGR- A004V28	125 A G ---	---	TCTAGCTATAAGACCAGATTTTAAATTTCTAGATATAGAATTATCCAGAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATATGATTATCTTCACATGA[A/G]AAGGT TTCAGTTATAAATGCTTAAATACGTATCTATTGCTTAAATACGTATCTATTGG
TGR- A004V28 a	29 A G CGATCTC	CGGAGGTTGCA GTGAGC	CCAGGCTATAATGTTGGGGTGGCATCT[C/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCACCTAACTAATTTTGG TATTTTGTAGTAGACATTTGATTTTGTAGTAGACACAGG
TGR- A004X20	25 T C GA	GAGAC	TAAGTTTCTCTCTCTCTGTAGGA[T/C]GCTCCATGTTACAGTCAACTATAAAACATGGGCTCATGT TCACCTGGGCTTCGCTTCAGAGGAGTTGATAATTTGGAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTCTTCAATTTCTTCAAGGCTTCTTCCAAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCCT
TGR- A004X30	26 T C CCAC	CTATTTT	TTTTGAAATCTTAGAGTAGAACCCAC[T/C]ACTAGTAATACITGTAAATAAAATTAAGTTT AAACACTTCCATAAAGAAATTAGGGTGCCAGCTCCTTGATTTCCCCCTAGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TGR- A004Z04	102 T G ATGCAAACT	AAGCAA	CACGGTATAGCCTTATATATAGGTATATATACAGATCGTACACAATATATTAACAGTTTGACATG GGGTCACAGTACCTTCATTTGGGTATGCAAAACT[T/G]TTGCTTTCATGAAATTTCTAATTAAAGG ACTGTGCTTCTTCATATTCATGGACATTTATACAAAATAACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C	T	GAGACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAGTTATTGGAGGAGCTTGACACCCCTCTCTGCGCTAGCTTGAGAGAACAACTGCG AGCATTTTTTCTTTTTC/TCTCCGATGACCATCTTTTGGGCTGGCGGCCAGGCCCTGGGTGTC TCCATATCGCTGCTTTTAGTGAGACTGAGGATCTGGTATAAGGAACAGATC
TIGR- A004Z42c	89 C	T	TTGGGGAGGT AGGAGACT	CAGGGCTGCCG GTCC	GTCTAGCAGAGGAGATACTTTGAGGACAGCCCCAACGGCCAGGTAGCCTTCAGGGGCGGGCA GGTTGGGGAGGTAGGAGACTCTTGAGCCGACGCTTGAGCCGACGCTGGCTCCAGCTTCATCTGTGTCCTT CATCATCTGTGCTCTC
TIGR- A005D17 c	81 T	C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCACAGCAAGGCTCTGTCTAGATCTCTTGGCTCTCTGTGAGGATCTCTCTCTGCGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTACGACAGTCAAACCTTACGACAGTCAAACAC
TIGR- A005D17 b	79 G	C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCACAGCAAGGCTCTGTCTAGATCTCTTGGCTCTCTGTGAGGATCTCTCTCTGCGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTACGACAGTCAAACCTTACGACAGTCAAACAC
TIGR- A005D44	97 G	T	TTAACATTAT GAACCTTAAA CTGTACAC	TTGTCTATTAT TTAAAGCCCAAC AAAA	CATCAGTAACATATACACAAATGGTCAATCAACTGAACCTTGCTCCCAATATATTTCTATACAATAGTT AACATTTATGAACCTTAAACCTGTACACTG/TCTTTTGTGGCTTTAAATAATAGACAATGATTTTTTG TCTATTACTTAGTGATAGACAAAGTGAATTACTTTTGTAGACAAAGTGAATTACTTTGTTAC
TIGR- A005E31b	27 G	A	---	---	GGAGTTCAAATTTATAACCAGGCCCTCTG/AJCTACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACTGCCCTGCCATGTGGATAGTACTCTTTGCGCTGCTTGCCCTACAAAGCCACTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G	C	---	---	CTCAGTGTAACAACTTTGTTTAGGGAAAAAATAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGCTGAGACAGAAATGACCCCTTGGGCTCCTTTATTTGTCTTTTCAACAGGACC CCACAGATATTGGGGTATGTCATGAGGACTGGGATGCTTCTATTTG/C/GGATGCTCTCTATTTT
TIGR- A005E42a	42 A	G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTATAGTAGGTTACTGCACCTTACAGAGTCAATTTCCCTGATTTAGGA AGGCGATGCTAATGGGTATGTCATAGGTGAATATAAAATGTTGTATTTAAGAGATCCCCACAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAAATAG
TIGR- A005E46	76 A	G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATAGTATTAGCCTACCGTTTGTAAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC/AGTTACATTACCTCAGACGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTTG ACAC
U120979	24 C	T	GCAGGGGTGA CGTATGTAGA CTA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/C/TGGCTTAGGGTGTCTCCCCACAGAGGAGATACCTTGAACCG ACTCAATTCCTGTGTAAAGAGACACTTTGTCTGCTTTCACGGACCTCCCCAAAGTGTGCAGAGTCTAT ATAGGATGCTGGATTAGTTCCTTTGATTTGTAAAAATTTCCCCAAAGAGCCGCATATGAATCTGCCCC

X57830	106	GCCT	AGTGGAAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCACTGTGGAAGGCACACTGAGCAAGTTTACCTATCTGTGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGAACCAACGATCATATCTGCTATGCCTCATTTTATCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGCTTGGAAAATGTTCTGACAGCATTTAGCTGTGAG CTTTC
X74070b	72	TGTGGATC	CTTTTAAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATCTG/GATAAAATCTAGATCTCTAATATTTTAAAGCCAAAGCCCTTGGACACTGCAGCTCTTT CAGTTTTGCTTATACACAATTCATTTCTTGACGCTAATTAAGCCGAAGAGCCCTGGGAATCAAGTTT GAA
Z48804	44	CT---		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGTCTCATCACCAAGCTTCTCCGGAAGGG CCTTAGGATAGGAGAAAGGTTTCATGCACACACGCTGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAAGG TCCA
D28513b	133	AG---		---	ATGACCAAGCCACCACATTTAGAACCTTTGGCTGCCCTTGGAAAGTCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTGTGACTGCATGAATGCIW GJTGCGGTGAAGCATGAACCTTTGTTAATCAAGAGGCTTACATAATTTTAAACAGTTCTGTCTTC AGCTGTACATA
D29833b	85	AG---		---	CCACTCCATCCTGATGCCCCCAAGTTATCCACAGCCTCCTCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAAAGTCTCCAACTGATCCTACCTCCCTACTCCTGACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	AG---		---	CCACTCCATCCTGATGCCCCAAGTGTATCCACAGCCTCCTCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAACTGATCCTACCTCCCTACTCCTGACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	GAT---		---	CTCCCTGCCTCCTCCTCCTGCCTGTGATGCTCCGCTCAAAACAGCCGAAACCTGCTTGTGAATGGGG GAGGGGGCGTTTGGAGCTTCTTCTTCTTGGCTTCTTATTCCTCACAACCACTTCTCAATAAA GCCAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGCTCCTCCTGCTGCTGCTGCTGCTGCTGCTTTT CTGGA
D37931	64	TTCTC---		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGT/CJ CCCAGGCTCTGCTCCTCAGCTCAITTCCTACTCTTTTCTCTATATACTCATTTCTATAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAATGAGGCTGGGCTTTTCTGTAAAGCTTCC TTT

D63807	101	C T ---				CAGCAGGACTTCAGTGCAGTATCCCTCCCTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTAGAGGGAGTGATTTTCTCTGTTCCA/C/TAAGAGGAGACTTTTGTTCACAAATGGATCAC AATGCAAGGAGTCTGTTCTCCCTCCCTCGGCTCTCGGCTGGGAGGGTGACCTGCCAGATGAC
D90145	21	T C ---				TGGAACTGGGTGAGCTCT/CJACAGCTACCTCTCTATGGACTGGTTATGGCCAAACAGCCACA CTGTGGGACTCTTCTTAACITAAATTTAATTTATTTATCTATTTAGTTTATATAATTTTATTTTGAT TTCACAGTGTGTTGTGATTGTTGCTCTGAGAGTCCCTCGTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035	59	T C ---				ATTACACTCTCAAAATTTTGGTGTGIGITTAAGTACTTCTTATTTATGAGCCCT/CJGAGGA CCAGACATGTTATTCAAGCCCTTATATACCATCTAAT
EST16668	71	C T ---				GCATTTTAAATTCACATTCATTAATTTACTATTTATGATGTTTACATAACAATTCAGTATCAT ATGIC/TJGTAGATTTACAGATGTAGTGTCAATCTAGGACCTTATCT
EST16904	57	C T ---				ACAGACTATCGCCAACCTTATAATGCTTAACTTTATGATCAATAGTAATAATTAACA/C/TJGAGATA TTCACACTTTATTATAAATAGGGTTTGTGAAGATGATTTTCCCAACTGTAGGTTAACAAT
EST21863	49	A G ---				TTTTAAGTACCAGAGGACTGCTGGACAGGATGAAACTGATACACCC/GJGTACTACTTACTC TTCACTCTCAAACTGATCCCTAAAGACTTCTACTTAGCANA
EST21885	80	GA ---				GGCTGAAGTAGAATCAVAGGTAAAGAACATTTTATGCACTTATCCACAAACATTTACTGAGCATA CTAGGTGCTGGG/GJ/TGTGACAGTGTGACAAAACACAA
EST22623	26	A G ---				ATTTAGTGCAATGACAAAGCCCA/GJAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCATAGATATACGAAGTTAACACAAAGTATGGGAGT
EST22644	98	A G ---				AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTTACAG/GJAAATGTGGAAGATGGCTTTTAAACCC
EST23587	31	T A ---				CCCTCATTTTAAAGAGCGGACATAAAAA/TATATACAACAAAAACCCAAAGTCACATTTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST24246	106	T C ---				AAAGATCTGGCATTATTCACATCATCTAAATATTTGTAATTTCTTTCCATGAGTATTTTTC TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACCT/CJGAATAACCCATAGTTACAGAATTGG GTCTGTGAACCTCAAT
EST24308	45	A G ---				TAGTTTAAATTTCTGAACCTTTGGCTTATAAAATTTTCTCAACTT/GJCATTTAAAAATGTATCAAT GCACCTCTTCAGTAGTACCACATGAATAATATAAACCTCGTTC
EST24435	73	GA ---				CTTGAACCTCTGGTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/GJ/TGCCTGACCCACATTTCTTTATCCGATCTGTGTGAGGACATTCAGGTTGTTTC
EST25089	25	T C ---				TATTGTGCAATTATCAAAATGGTTA/CJAGTTTTCATTAATAAACTGTAATGATTCTTCTATGTATAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTGTTAGTTAATGCTACATT

EST25476 9	33 G A ---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAAN[G/A]CTTTCTCCTCCTCTAAAAAACCAACACA AGAGGTCCTCTTGCTGCCITTCATGGACTGTGGCGGCTGTGGACTTGGACCGCTGCTGA
EST26183 2	70 T A ---	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACCTTTGTAAAGATTGATCTCTAAATAAG ATT[A]ACATTCTGGGTACTGGGAGTTAGAACAC
EST27231 1a	28 T C ---	---	AGAAAATAAGGTGCTACCGAACTCATGT[C/G]ATAGCGCTTTCTTTAGGCACATATTATAGCAATT CAGATGAAAGTTCTGTAATCACACACACTGTGCTCTAACACAAACACGGTGACTCTGA
EST27816 5a	26 T C ---	---	CAACTCAAGGTACAAGACAATTGCAIT[C/G]TAACATTGTTATAAATAAAGGAACATCAGATCAAT CATTAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 A T ---	---	GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCAJA/TGGTAGAAGGCCAAAGAGAACGAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGAT
EST30226 5	25 A C ---	---	TACTCACCCGACATACATATCTCA[J/V]GTAGAATTAGCTATACTGCATACTAATTCACTTCCCTTGA AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCCCTTGA G
EST30935 9a	59 C G ---	---	AGCTATGGTAGAGCAAAATCCAGTGGTGGTAAATCAAGAAGCTCTAAAGTTCAGTAGAG[C/G]AGGT GTTTGAATGTCAAGGAAATCACTAGGAGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTGTGAGG
EST32515 7	25 G A ---	---	CCGAATATAAGGAAAAATGGTGGC[G/A]TGCCCTCTAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCACITTCCTATGAATACTGGCACTGTTTATTTCATGTTTATATGTGAGTTCTATGC ATAAAATCCCAGTAAGA
EST33274 4	27 T C ---	---	TGCTTGTTCCTCCAAATCCTAAAAT[C/G]GTGTCTTCAAAGAAATTCGTGGAAGGACTTTGAA TACGAGTTTGACCATATTCAAAGTATCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCAT GGACTAGGTA
EST33352 7b	75 C G ---	---	TACACATTATCAAGAGACCACCTGACATGCATCTCCTCCGAGAAATACATTTCGCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTACTAAGAGAAATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 A C ---	---	ATTTTCCCACAGCAGAAGTATATTTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTGG GAACCAAGTACAGAAATGTTACAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAGGTGTGAATCCTCTT
EST33488 7	90 A G ---	---	CCTTTGGGGAGTTTTAAGCCAGAAATGTGACAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG TTGAACCTAACATCGTCTATAG[J/G]ACCAATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 C T ---	---	AAAAACATGCTATTGAAACAAACTTTTTTATAAGAATAAGTTGA[C/T]TGAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---			AAAAATGCTATTTGAACAAACTTTTTTATAAAGA[A/G]TAAGTTGACTGAAAGCAGTTTTAAAT AACATCAACTACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTATTCTTGTTTTGAAAAAATTATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAAAC[C/T]CTTTGAACACTACAGCTGAATCCCCC
EST34739 3	97 T A ---			GAAATATCCTCCAGTGGCAGGAACGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTCTAGGCTGGGGAACTCT[A/G]GGTGCCTTACAACCTCCAACTACTGCAGAAATTTCT TGTTGGCCTCATAAACA
EST34792 6b	104 A G ---			ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCCTAGTCTATTACA AAGATTTGTTGCTGTG
EST34835 9b	93 T G ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGGT[G/G]GGCCTTAAAGAAACAGACAAATTTGTCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTG[A/G]TCTTCTGGTGCCCTTAAAGAAACAGACAAATTTGTCTAAAGAT
EST35230 0	93 G T ---			CACAAAGGTCACCTTACTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCT[C/G]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---			TCCTTTCAAAATTTTGATGAGGCATTTAATG[C/T]ATAAAATTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTGTTCCATTTTACTTAGTTCAGAACTTTTCAATTTTCATCT
EST35708 9	32 C T ---			CTGCCCCAAATTAACCTTTAGGCAATGGAA[C/T]AGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTCCCTCTCTGAGGTGGCACCTTTCCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGTCATTATATTAAACTGAGGGAACAACGGTGTGACATGGCAGACATTTATTCATGGAGA AGTTCTCCCATGAACCAAGA[C/A]CTTGCTCTCATGATAAAGTGGAGACAAATAAGAAAGCCAGGT ATATAATTAAGGCTGTGA
EST36301 4	93 C T ---			CACCTGTTCAATGTTCACTGGGCTGCTATCTGTTGGGCTGATGCTTACCAGGTGCTAGCCTACAGC AGTCAGAGGCGCAGCCATGGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCCAACTGATCTTCA GAAAGAGGTACACAAA
EST36519 0a	33 G T ---			GCCATCAGCCCCACAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTTAGTCGT

EST36620 6	50 G A ---	---	GAC TTATTAGATAAGGGGTTTCGGCTACCCCTCAAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTAAATATGGAAATAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---	---	CCTGTGATGTGCATGGGTCCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGGATTCTA[C/G]AGGGGACATATCACACATATCTTAAGTCACCTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 C T ---	---	GAGACAGAAGCCATCAGTTAAATGAGGTAGGCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	ACTGTCTGCCCGATGATTGGAGCTTGAAAAAATACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCTTCTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGTAATGGGAGATACCCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	GGTCTCACTCTCTTGGCCAGGACGGTTTGAACCTCTGAGCTCAAGTGACCTCCCACTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACACACACTGGTCTTGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	AATAGTCTATGGTACGGGCCGTGGGATGTTAAAAATTGGGATTTTAAATTAAAGATTGTGAACATG CAAAACCAGCAAAATTTCTCAGCTTATAATTTGAAAGTCT[G/C]CAGGAGAAAAAATGGGGTCC
EST37284 2	93 G T ---	---	AAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAGGAA GCTCTCTGGATAATGTCACCTCTAGGA[A/G]TAGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCT CTTGGCTTGCCTGAGGAATA
EST37315 2a	90 A G ---	---	AGATGGGGCTTGTAGCTTGCTCGGCTGAACTAAAGATATCCTCTGCCTCAGCCCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	CCTGCCATGATAATGTTAAAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAGCATACC ATTCCATTTAGTTGAAATATTCCTTCACATAGCCAACACATTTTTTCAAGGCACTCTAGTACTACA GGA
EST37376 8b	101 G C ---	---	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGTTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAATCACAGTGTCTGTCTCTGCA[G/C]GCTGTCTCAGGCAAGTGTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---	---	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGT[C/T]GAGCGCTGGGGCTGAAGTCAG ACTCTCTGGTTCAATCACAGTGTCTGTCTCTGAGGCTGTCCTCAGGCAAGTGTGACTTCTCTG GTCCAGG



EST37378 9	63 T G ---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCGTGAAAACT/G JAACATGCCTCAAAAAAGAGGGGAAAAAACITTAACAGAAAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---			AAGACATAAATCTGCAATGAAATCAGTTATGAATATAAACCTCTG/AJCTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCGCTTAAATCAATGACGTAGAA
EST37613 6	34 A G ---			CTAGGCATGGGGCTTTACAGTCATTTATTTAC/AJGJGTCATGAATTCATTAAACCACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAATCACCCCTGCGTTTCATGGATCTCCATTCTAA
EST38025 4	56 T G ---			TTATTAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACITTA/TGJTTATCTCA ACAATCTTGAAGGTGGTATTATTTCCCGGCTTATAGGIGMAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---			TCTACCAGGTCACCAAGATATCTGTATATGCTTTAAGTGGCATTTCATGTCACITTA/CJTCGCATGG AAGAACGCTCTCCTTTTAAITCCCTAACTCTCTCTCTGGAAGACAGAACGTCACAA
EST38420 6a	100 T C ---			TAAATCAAGGCCTCTTTTCAATACCAAAACAAACAAAAAGGGGAAACAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCATCCTGACTGAC/TGCTCCCTGCAGTGCCCATGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25 T C ---			TTTATTTGCAAAAGTAAGCAGCGGGT/CJTGCTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAGAGAAACAAAAGCTT ACAAACAAAGACAGCCA
EST39053 6	90 T C ---			TTTTTGTACTCTGTAGCCAGTCATTATCTGAAGGTTTAAATATATCATTTTATGGGATGAGATCA TAGCTTTACACAAATGCTATG/TJAACAAGTTACTGAATATTTTACCTCGTGGAGTTG
EST39331 1	70 G C ---			TCCTCTTGCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TG/GC/GJGTTTTAGGGAGAGCTGGCACCTGCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACACT
EST40544 7	31 C A ---			GTCACCATTTGACCTTACATAGTGCCTCTAGT/C/AJACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAATTT
EST40548 4	37 T C ---			TTCTAATAGCATGCCCTGTGACAGGGGAAACTAAGCTC/TCTCAAAATAACTGAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTCC AATAATCTGTGGGACTCA
EST40549 1	42 A G ---			TGTTTCTCTAGAGAACCCCTGTGTGATACACTAGGCATGCACA/AJATAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCATTTCTCATTGAACTAGTCCCTGCCAAAGCACCCTTCTA CCCTGCACCTTTTGGGAG
EST40579 1	81 A C ---			TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTTCTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAAAA/CJGGACTTGGAGACAGCGATTAAATACGGAAACAAAGGCTTCCAGGAAG
EST40584 3	68 A G ---			TTGTATGGTTGTAGGAATTTGGGAAGAAATTTATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A/AJGJCTGTACTCCCAATATCCTATGTTTTAAGCT

-228-

EST51340	51 G A ---	---	GATCAAACTGTAATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAACATAGAACTCAGAGCCAGATCCTTTATCCAACCTCTCGA T/CJTTCCTTGGTCTCCAGTGAAGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGT AGCTG
K01506	63 T C ---	---	CTGMCCTCAGCTGCCCTACAACTCCATCTCAGCTTTTCTCTCACTTCATGTGAAAACACTACT/CJC CAGTGGCTGACTGAATTTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCAATCCT TAGTAAAGTTTCCAACAATAAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCCTTC ATTGAGCCTTTTATCCT
L18877	69 T C ---	---	TGAGTCTGAGCAACAGTTGCAGCAGGGCCAGTGGAGGGAGTCTGGCCAGTGCACCTTCCAAGGCC C/T/CJATCCATTAGTTTCCACTGCCCTCGTGTGACATGAGGCCCATTTCTTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTTCTGTCTATGGATGACTTTGAGATTATCTTTGTTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	GCATTTTACATATCCCAAGCCCTTTAGGGCTACAGT/CJCTCTGTCTGTGACCCCTGTAGGGTGCCA TTTGGAGTTACAGCCTAGAGGAAGAAAGGCTTTGGCCCTGGTGGTGCCATAGGCCTGTATATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT GT
L38517	137 G C ---	---	GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGAACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGCAACACCAGCGTCCCCAC CC/G/CJCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---	---	ACTTGAGAMGCAAGCTCGCCACCTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAATAACAGTAGTATTTCTTTTGTATTTTGTATATT/GJGCGCTGA AGATCATCCGCAAGGCAAGGCTGGAGGTGCGGTGGCCCTGTGTCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	CAAAGTTGCTCTCTGCCATGAGCACCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAGTGGTTGCCAGCTCCAAATGTACCAGCAGCTGGAATCTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTCTCCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111 T C ---	---	---	AAGTGAACAGAAAGCAAGATGGATTGTTGCTATATAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAAGAGCTCAAGTTTTTGGTTTACTTTTCAGAAAT/CJGAAGAACATTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCTGTACCTTGAGATCCA
M18079	52 G A ---	---	---	GTC GCGACAGTCCAAATACAAATTGGACAGAAGATCTATATTGTACCAAGAACT[G/A]TTTATTTCACC CCATCAAGTATAAGGTTACTGATTGATTGGTCTTTTAAACATTGGTATATTCCATTTCATGCCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113 T C ---	---	---	TAGGGATCTGTGCCAGGCCATTGCGACACGCCACCCCACTCCACCCCTGTAGTGCTCCACCC TGGACTGGTGGCCCCACCCCTGGGGAGGCCCTCCCATGTGCTGT/CJGCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCCCTTTGTTGCTCAGCAGGGCGCTCCGCCCTCCCTCTCTCTCTCTCTAATA GC
M21539	114 T G ---	---	---	TCACCTCGTTCCACAGCTCCACCTGCATCTTCTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCCTTAGCCTGTGATCTGCCCATGATGATCCCGACAGCAAAAT/GJGTTTCCCTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCCCTTCAGAGCT TCTCTTGGGTGC
M26041c	173 A G ---	---	---	CCTAGCATATTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTTCCCTGACTTC CTGATTTTCTCTTCTCAAGTGTACCTACTMAG/GJGATGCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	---	CCTAGCATATTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTTCCCTGACTTC CTGATTTTCTCTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	---	CCTAGCATATTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTTCCCTGACTTC TCTGATTTTCTCTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	---	TAAGGCAGCTGTCAGGGAGGCCAGTCCAGATCCAGCAATTCACAACCCCTTGAC[G/C]AATGCT TGCCAAGCTGTTTAAAGCCCAAGAACACCCCTTTCTTTGTTCCAAATTAACCTTAGAAGAAACCCCA CAAAATAAGCAATTCATC
M81695	34 G A ---	---	---	ACTTACTTACCCTACCTGTACGGTGCAGGGGAG/GJGAACCACTGCACCACCGAGAGAGGCTGGG ATGGGCCCTGCTCTCTGCTTTGGGAGAAACGCTGCTGGGAGGGGCCCTTGTCTGTCAAGGTTG CAACTGGAAACCCCTAGGACAGGGTCCCTGCTGTGTTCCCCAAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166 C T ---	---	CTCC'CCCTTATTTCAGCATGGAGGTTAAATGGAGGATCTCCTTTCCCTGTGACAAAACATCTTTC ACAACCTACCTTGTAAAGACAATTTAAAAAGATCTTTCAACAACCTTACCTTGTAAAGACAAAAT TATTTCCAGGCTATTAAACGTACTTTAG[C/T]GGAATTATTCTATGTCAAATGATTTTAAAGCTA TGAAATACAAATGGGGGA
U09607	39 T C ---	---	GAGGCTTATGAGGTCCTCTACTCAGGAACACCCCA[C/T]GACATTGCAATTTGGGGGGCTCCCG TGCCCTGTAGATAGCCTGTGGCCTTGCATTTGTAAGTTCAAGACAGATGGGCATATGTGTACAG TGGGGCTCTCTGAGTCCTGGCCCAAGGAAGCAAGGAACCAAAATTTAAGACTCTCGCATCTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAGGCAAGAGCGGCAAGATGATTTTGAGCGTTGTATCCAAAGGCTCATCTGGAGCCTC GGGAAAGTCTGGTC[C/T]ACATCTGCCCGGCCCTTCCAGCCCTTCCCCAGCCCTCCTCTGTGTTCTTC ATTCAATCAACAAAATTTGGC
U10694	20 C G ---	---	GTGACATGAGGCCCATCTT[C/G]GCTCTGTGTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGTCTCTTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTTAAATGGTCAGTTTAAATGAACCTTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAGGACTCTGGTTCAAAATCCAGTTCCATTTTGCTATCTTTGTACCTTGCACAACTGTTTAAAC CTCTTTGTCAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATTAGTGAAGTTACATGT AAGCACAGAGGAACAGCCCAAGAGAT[C/T]TACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187 T C ---	---	TTTCTGTCCACTTTTACCTGGTTTAAATAGCCAGCCAGTCATAATAGTAGGGAATCAGTCAAGCAA AAATGCTTTGGAAGAATTAAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACAGCCCTTTTCTAAGCAGTCTGGTCCATG[C/T]GGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122 T C ---	---	TCCAATTATGGTCCCAAAAGCAGCTTCCACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTACAGAAGCTCCTTGACAGACTGAGCGATGACACCACAC[C/T]TTGTTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTGGGAAAAACAACCTGCTCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAAATAGACTCAGCCTATGTCTCTGATTCCAGCTGGGTAGTCTAGAACTTT[C/J]AGAAG CTCCATCTTTTAAATGTTTATTGTTATGTCCCCCTCCCGGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACAGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACCTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164 C A ---	---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTCTACAAGAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAC/C/AJAGATATGACTTTTATATGAACCCCTTCTTAGG GTCCAGAGGAATTGTGGACTGA
U25975a	143 C G ---	---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTCTACAAGAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAGCAATGACTATTCTCTG AAGACAAC/C/G/JAAGAGAAAAATTGCAAAAAGACAAATATGACTTTTATATGAACCCCTTCTTAGG GTCCAGAGGAATTGTGGACTGA
U25997	61 A G ---	---	---	CAGGAGAGGTTATTACAACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTTATTTTAAAGTAGTCCCTATTTCTATCCCTTTAAAGAAAAATT GCATGAACCTAGGCTTCTGTATCAATATCCCAACATCTGCAATGGCAGCATTCCTCCACCAACAAAA TOC
U28413	29 C T ---	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/TTGGGTAATATTTTCTCTCATGTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTAGTCAAAATGTGTCTTGTATCC CAGATGTTGTGGCCTGGAAAGCCCTCATTTGCTACAGTACAAAGTAACAAGTCGTTGTACCTCAGTT G TAGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTATGATTTTGGACCTGCCGTATATCTGTT CTTCTATCCACGTTAGCCAA[G/J]TTCTTGTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAGT GCTGTCA
U30884c	89 A G ---	---	---	TAGGGTAGCATTTAAGATTCAGGAGTCATTAGC[J/G]GTGATGATTTTGGACCTGCCGTATAATCT GTTCTTCTATTTCCACGTTAGCCAAATGTTCTTGTATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAGT GCTGTCA
U30884a	34 A G ---	---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCATGAGACGGCTGCAACCAACA GCCGTCTCAAA[G/J]CCCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTTACACGTAGAGGAGGAGGATGCCACAGCCGATTGCGTTTAGCCCCGCC TGGTAGCCCTTCCAT
U31216b	78 A G ---	---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCATGAGACGGCTGCAACCAACA GCC[G/J]TCATAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTTACACGTAGAGGAGGAGGATGCCACAGCCGATTGCGTTTAGCCCCGCC TGGTAGCCCTTCCAT
U31216a	70 G A ---	---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCATGAGACGGCTGCAACCAACA GCC[G/J]TCATAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTTACACGTAGAGGAGGAGGATGCCACAGCCGATTGCGTTTAGCCCCGCC TGGTAGCCCTTCCAT

U31416c	76 GA ---	---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCACGAGCACAATCTGGTGCCTCTCTCTGCTTACAAATGCTAGGTCCTCCCACTGCCTGCT GGAAGAAACACACTCCTTTGCTTAGCCCAACAGTTCTCCATTCACTTGACCCCTGCCCACTCTCC AACTAAGTGGCTTACTCTCT
U31416b	68 CT ---	---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCAGCCCAAAATCTGGTGCCTCTCTCTGCTTACAAATGCTAGGTCCTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCCAACAGTTCTCCATTCACTTGACCCCTGCCCACTCTCCA ACCTAAGTGGCTTACTCTCT
U37519a	78 CT ---	---	---	ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCTCTCC AGACCGCAGG[C/T]TCCCCAGCCTCAGGTTGCTGGAGCTGCACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGCTTGTCTTCTATCTGGGGGACGCTGCTCGAGAGAGCGCGAGAGGCCGAGAAC ATGCCAGGTGTCC
U37690	54 AG ---	---	---	GACCACGCTGAAACCCACCCACCCGCTGTGCTGAACATGGGGCCTGAGGTCCTT[G/C]CCCCGAATTC ACGAGGCTGAGGCATCCGGAGCTGGGTAATGCCTGGCCGACGTGTGTGTAATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAGGTCCTT
V00540	39 TC ---	---	---	TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAAT[C]ACACCACTGCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCAACGCTAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAAGGCACTAGTCCCTTACAGATGACCATGCTGAT A
X15943	106 AT ---	---	---	TCAAGAGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACCTCTGAGCCTCTCTGAGACCATGTGGTTTTTAAAA[T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTCCAGTAGCTAAGACCCTAGAATTTGGATTCACTCTCTGTTTTTTCATGCTCTCCTT GTAAACCCCTGAGATCATCAG
X52011b	148 CT ---	---	---	AGGAAGATCCCACCGACCCCTTCTGGCCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAGGAGACACATTCACAAAGAAAGTTGGGAAATTTGCG AAATCTGTTGTGCA[C/T]GCTCMAATGAAACGCCCTTTCGGCTTTGGCTTTATTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 AC ---	---	---	AGGAAGATCCCACCGACCCCTTCTGGCCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAGGAGACACATTCACAAAGAA[T/C]GTTGCGAAATTT GCGAAATCTGTTGTGCAAGCTCAATGAAACGCCCTTTCGGCTTTGGCTTTATTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT



[illegible]



1282	130 C T ---	GTGGATACCACTACAGTCTAATTTTCAGATGTTTTCATTACCCCTAAAAGAAATCTTGACCCATTAGCAATTCCTGCTATCTGCCCTCACCCCGCCCTACTCTTTATCGTATAGATTTGCC[CT]ACTTGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTTGGCTCTTTCACTGAGAATAATGTTTCAAGGT
6810	68 C T ---	AGTATCACACATACCTTAATATATTAGATATACACATAATAAATCACTCCCTACCTTGAAACATTTA/C[CT]AGAAAGCATTTTAAATTTACAACACAAGCTCAAAAGAACCTACAAATAGTCTAGTAGCTGTGTTACGTGCCAAGGATAAGGCTGAACAATAAATTAACCCCTTTAAAATGCTATGAACAAGTACAAATTTCTTTTGGAGTTCTGCAGAGCAATGACCACCTAAGAAATATTTTAAAGGC
6817	118 A C ---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCAATCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGAGGTAAC[A/C]TGTGGATACCCCTGTGTGCTACTGGCCTCCAAAGGCATTCAGGGGATCATCAAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGGGCTGTGCAGATCGGCTTTTGGTTGGTTGCTTAG
6819b	212 C ---	CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAACATTTAGTACCATCATGTGACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTTTCATATACAAAATTTCTGCTATTTTGTCTTTAGCAAAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166 G T ---	CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAACATTTAGTACCATCATGTGACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATTTTGTCTTAGCAAAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G ---	CTGGTATGTCATAAGCAATCCATAATTTGTTATAGCTATT[A/G]TTACTATGGCACCACTTTGGGACACAGATTATATATGTCAGACACCAACGAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTTAAACAAAGAAATGAACGCTAGG
6972b	149 G T ---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGTCCCTGGACTCTTTTGGTTGGTAAACTATGATTATGGCACAAATTCAGA[G/T]CCTGTTATTGGTCTATTCAGAGATCAACTCTTCTCTGGTTAGTCTTGGGAGAGTGTATGTCTCGAGGAAT
6972a	122 A G ---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGTCCCTGGACTCTTTTGGTTGGTAA[G/CT]ATTGATTATTGCCACAAATTCAGAGCCTGTTATTGGTCTATTCAGAGATCAACTCTTCTCTGGTTAGTCTTGGGAGAGTGTATGTCTCGAGGAAT

7598k	210 A C ...			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CAATGCAG[A/C]
7598j	208 A T ...			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CAATGC[A/T]GA
7598i	192 G T ...			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CCTCAATGCAGA
7598h	144 C T ...			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ...			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]CCATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ...			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ...			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ...			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACCAAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATATGATTTACAAAAGACACCCAAAGCCA/GJAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATATGATTTACAAAAGACA/CJCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTA/GJTGATTTACAAAAGACACCCAAAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAATGAATGGGTAGTCTATCTTCTCAAGGTCCTCCCAATAA/TJCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAATGAATGGGTGCTAGTCTA/CJCTTCAAGGTCCTCCCAATAA/TJCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAATGAATGGGTGCTAGTCTATCTTCTCAAGGTCCTCCCAATAA/TJCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTAAGAACTGTTTAAAGTAGAAAAAACCTGTCAAGAAAGACCCAGGTGG AAAATGGTTCCCAATAAATGGAATTTTAGGGCAACAAAAGTCTAAAGGCC/GJCAAAAAGAGA AATAGCACCACTGTCAATTTGAACAAATGGCTAGTTACTTGCAATTTTGGCATTTGTTAATCACTGAATC TGGGTTTCTCTGAAATCCACACAGAGCATGCACCTACACAACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTCTCTAAACATCAGTCC/TACGGAGAAACTGGGAAAATCCTGGATATTTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTA/CJ/TGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTAAGTCTG
8467a	70 A G ---	---	AAGGCTTCTCTAAACATCAGTCC/TACGGAGAAACTGGGAAAATCCTGGATATTTGGCTTATCATT TG/GJCGCAAAATCCACTTTGCTGTAACTGTAACGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTAAGTCTG
8498	84 C T ---	---	AGGGTTCAAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG/CJ/TAACTTCAATTAATCGAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCTCAATACAGAACCCAGGAATGTAATTTTCTTAAGTCTG

WI-18562	29 GA ---	---	---	CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTTCTTACATT TAGCATTATCAGAAACGA
WI-18618	51 AC ---	---	---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGTAAATTTGTAAACCACAGTGCTCGCACAGTTC AC
WI-18683	22 CT ---	---	---	TAGCTGTTCCAGGACTGGACTC[C/T]GGTCCCTTTATTAGAGACTGACAGGCCAGTGGGTCCACCCAAV CAAAATAAATTTCTCTCCAAAGCCTGCCTGCAGT
WI-18520	75 GA ---	---	---	GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTAACCCTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCTCTCCGTGAGAC
WI-18563	94 AG ---	---	---	AAATAAGTTTTATTGGCACACAGCCAAAGCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTCACTAATGTGAC[G/A]GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69 TA ---	---	---	GTCTATTCAATTTAGCTAGACCCATTTCATCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC T[A/GT]GCCATAATTTAATCAGTGCCATATTGAAGACATTTGGATCGTTCCAG
WI-18723f	94 GA ---	---	---	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCTATCCACATTTGACTGCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAA[G/A]TATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71 TC ---	---	---	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCTATCCACATTTGACTGCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96 AG ---	---	---	TTTATTACAATATTAGGTGGCACATAACTAAACAGCTTCTGA[G/A]ACAGGAGGTAACATTTCTCA TAGACTTTGCAACTCAGCCAGAAGTAAACTCGAAATA
WI-18619	44 GA ---	---	---	TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAGGGAGCCTCCAGGTGGAAGGTTATTTTAAATAAAAAATAA
WI-18715	76 GA ---	---	---	TGGAGCTACAACACACCC
WI-18535	107 GA ---	---	---	GTAATAAAGTTTTATTGGCACAGCCACGCTCGTTTCATTCATATGCCATGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTAAAGCAGTGGTCCCAAC CTTCTGTGGTCCCGGTG
D17525	107 CT ---	---	---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTACTAGTTTTCACTTCTGGCAGGTGAC TTCATCTCTTCGAACCTCAGTTTCTTCATAGATGGAAG[C/T]GCTATACCTTACCTCGTAAAA GTCTGATGAGGAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGCTGTCTACCAGGCAGACGAAG

DWU-133c	313 A G ...	...	...	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGCTCATGACTTTTATGTGTTACCATCCT TTAATAGATCTATACACCAGAAATCAGATCATGAATGACTGACAGAAATATTTTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236 T C ...	...	...	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGCTCATGACTTTTATGTGTTACCATCCT TTAATAGATCTATACACCAGAAATCAGATCATGAATGACTGACAGAAATATTTTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199 C T ...	...	...	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGCTCATGACTTTTATGTGTTACCATCCT TTAATAGATCTATACACCAGAAATCAGATCATGAATGACTGACAGAAATATTTTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC ITCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102 C T ...	...	...	ATGAGATCCTTTAAATCCTTCCATGAACGTTTGTGGTGGCCACTCTACGTCACAAATGAAGTG TGTTTCTTCAGTGATCTGGGAAGATTCTACCCCTTGACCAACAGATTCCTCAGCTTCCATTTGGCC CCTCATTTATCCCTCAACCCAGCCACAGGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATAGACCATAAAGGGAAGGATTCTGTGGAATATAAAGAT
DWU-387	169 G T ...	...	...	GTGTATAAATGCAACTGTTGATTCTCTCAACATGGCTCACAAATTTCTATCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCCTGCCAACAAGTTCACCTCATATATAAAGCATTTATTTTA CTCTTTGAGGTGAATATAATTTATATTACAAATGCTTAAAGCTTCTTAAATACTAAGTATTTTCA GGTCTTACCACCAAGTATCAAGTAATAACACAAATGAAGTGTCTATTATCAA
DWU-447b	172 ...	...	...	ATTTTAGTGCTTTTGGTTAAAAATCATTGCAAAAGTATTCTGAACGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT CCATTATTTTTCATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAAATGCTTTCTGTTAG GCCCTTCTTCTTACATGAAGAGATGATCTTCTAGTTTATGGTTA
DWU-447	85 A G ...	...	...	ATTTTAGTGCTTTTGGTTAAAAATCATTGCAAAAGTATTCTGAACGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATGATCACTGTAATTAATTAATTAATTAATTAATTAATTAATTAAT CAACCATATTTTTCATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAAATGCTTTCTGTTAG TTAGGCCCTTCTTCTTACATGAAGAGATGATCTTCTAGTTTATGGTTA
DWU-476	63 C G ...	...	...	GTAAATTCAGTTTTTCCAGTTCTCTTTTGTGCTGCTTCTCAATTAAGCGTTTAAAGTGAGTC/GAT AAATCAACTGTCATCAGGTGAGGTGCTGCTCCATACCCAGCGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAATCTATACCATACAAAATTTAA ATTTGACAGTATTTATGTTTAAAGCACAGGTGTACCGAAAAGTGTGAAGTCTGAATTTATGGGTT CTATGCATGCAATTTTGCCTAACCTAGAGAAAGAGTTTGATAAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGTACTTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	---	AAATCCAGGCAATTCGAATCTGTTTTCAATGATTTATAGAGGTTTACAAAAGTGCCACTTATTAA AGAGCTCCACAGTGAAGATGGAAGAGGTGAACCTGCTTTGAATATCCAGATGTTTTGGTC[AG] TGCGTATGGCAGTGAGCAGGTATGTTTTGCTTTGCTTGCACTGAAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTTTATTCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	---	AACTGCATATAGATAATTATCCAGGATGTGGCTCATCTTTTCAGCTTGTCTTCTACTGTTTGT ATATACAGTTTTGTAAACCATATGATTGA/CJAAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAATAACATATCTTCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAATCTAGTCCTGATTTC
DWU-59	94 C T ---	---	---	CATTCTTTGTAAAGGTAATGGACTCACAGGGGGAAGAAACATGCTGAGAAATGGAAGTCTACCGG CCCTTCTTTGTGAACGTACATTTGGC/CJTAGCCGTGTTCCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTGTTTTAACTTCCAAAGGTGTTTTACTTCTGATAGCCGGTGATTTTCCCTCCTAGCAGACATG CCACACGGGTAAAGACTCTGAGCTTCTAGTGGTTAAGC
EST11	68 C ---	---	---	CTTGATCATGGGTGGAAATTTTGTATCTGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	---	CACACTGGCATCTAGGCCTTCGGCTGCATTGCAGAAGGAGAGCCAGTCCCTCCTGGAGAA/CJTG CTGGTTCCCCAGCCCCACCCGGCTTTGCACCACACAGGCTTTGAGGCAGGAGGTGGGTAAAGAGT AGCTGTAGACCCCAAGCAACCAACCCAGCCCTGGGACCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA/CJGAATGAAAGTGCACCATCAGAGT GTAATTAGGCTCTGTGTGACCCAGGAAGTGTCTGTTAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAAACTTCTAGAAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTAATCTTTCATAA/CJCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT/CJAAACTTCTAGAAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTAATCTTTCATATACTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	---	TGTAAGGTGACTTCTATAGCTTCCCTAACTGTCAAACCTTCTTACTGAGATTTTTCAGGCCAAT GTGTC/JTGTGGTCTGAGATTTGATTATCAGCTGGGTAAAGTTAACCTGTTCCTGTTTCA

WI-18063	105	G A ---				AGGCTTTAAACTGATACAAATTTGCCTTTAATCACATACAAAACCTCTGCACATTCATTCCTTCCTTC CCATGTTTCTGATTGTGATGTAAACCTTAAATTTGTG[A]TCCCTTTAACAAATACTGTAGCTGCA
WI-18078	86	A T ---				AGTTGAAAGATCAGAGAGGTATGGTTGGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTG TTGTTTTCAGCATCAG[A]TGTCCACTAGCCAAAGTTGATCTGCAGTATACATGTGGT
WI-18091	90	T C ---				CCAAAGCTCACTCACTATTTAATCATCTGCTAATTCATCCTTTGTTAATTCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGAATTTGACCTTTCGGGCCCTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18119	38	T C ---				GCAATCTGTAAACAGTTTGGTAGTGGTATTACAGAGGA[T]CTGTGTAATGGATTGGAGTACTTAC CACTATTTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAAATTTGGTCTT
WI-18142	66	T G ---				TTCAAGATTAATTACAATTGGAAGGGGACCAATAATTCACATTTTAAATCGAAAATAATCTATATAQ TGTCCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	T C ---				GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCCAGATTCACTCCATGCCCTGGAGGTAGTCTGGGGG GTTCGGCGGGATGGACACACAGACAGACATAGATCTGGCATCTGTAGCAGGGGCATACAG
WI-18244	35	G T ---				TCAATCTGAAAACCTGCTGTAGCCAGCATGGGT[G]TGGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACACAGTACAGGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A ---				ACAGATGTCAGTTGTTGAATGGCCCCATTAAAGTATGGGGCTTTCTGTTAAAAGTCATCCAAA AGGCTTGGCAAGATTGCTATACAACGGAGGGACAGAGAAACATGA[G]CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18261	26	G A ---				GATTGAAGGGATTGCTTTATTAACTG[A]TGMAAAGCGTGATAGAGGAACTGTTTAAGATAAACAA CTTATAAATACTCCCAATTTGTAGAAGTGAAGATTG
WI-18268	88	C T ---				TAGGAGGGAAAGGAGGTGGCTGCTGGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC TTCCTTACTTCCCCCATAGATCTCTGACAAATGTCTGCAGAGCCCTCCAACCTGGAAC
WI-18299f	107	C A ---				TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGGCAATTTTTT ATCTATTTGGGCTGAGAAATCCACAAATTTTG[A]GAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299e	101	A G ---				TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGGCAATTTTTT ATCTATTTG[A]GTCTGAGAAATCCACAAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299d	77	G A ---				TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGGCAATTTTTT TGTATCTATTTGGGCTGAGAAATCCACAAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299c	67	T G ---				TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGGCAATTTTTT TGTATCTATTTGGGCTGAGAAATCCACAAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG

WI-18299b	52 GA	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTTGTCTAAGATCATTAACCTG/AJTTCGCAATTTT TTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATTAATTGACATATTCTG CAG
WI-18299a	48 CT	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAAC/AJTTGGTTTGCCAAATTT TTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATTAATTGACATATTCTG CAG
WI-18307	76 GA	---	---	TCAACTGTACCAAGTTTAGCAGCAGAGGATACTCTCTAGAGACTTTCAGTGGACTTAAACTCAG TTTCGGCTG/AJTGCTATGTAAAGCATCCACGATGGTTTTATGTACTCTGCAATCTGCTTTGGTTCAC TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAACTCCGGGGGTGGGTACTGAT TATC/CJTTAGATCCAAATAAGCATGCAGAAAGTG
WI-18324	72 CT	---	---	ATGAAAGTCACCTCAATCATAGGGTCAAGAGAAAGAAATGTTTTTCAGAT/CJTAAATCTATGAA GGTGTATCTGCTTGCATTTAAGAAACAACACAAAGTCA
WI-18350	48 TC	---	---	TCTTGACATGATCTGAAATAACGTGATTGGTTGAAATTCCTGGAAATTTGAAGAATAAATTG ATTATTCAAAG/CJTGTCATTGGTTTTATACATATCTCCTCTCTTAATGCAAGCTATG
WI-18395	77 GC	---	---	TGCAGTGGCAAGACACCTCTCGAGGAAAAAAGAAAAAGAAAAACAACCTCAAGGGTT[G/T] GATAACATTGCCAGTAAACCATAAATTCAAAACAGCAGCAAAATTTGGAGGATAATTTGT
WI-18398	62 GT	---	---	CTCGTTGGTATCTCTCATCC/C/AJTTCCTTTTCGCTCTTCTAATAATTAAGAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACTTTAACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18396	21 CA	---	---	AAGATGGGAAAGAGGAAATC/C/AJTTCCTTACTAGAGATTTTTTCCCTTTAATCCTTTTCAAA TCAAGGATCATCAAGGAGCAGGTGCAGAAAGCTCTGGGGCCAGAGGCCCAAGTGCTA
WI-18409a	20 CA	---	---	AAAAAGGAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAAAATAAGTTTCTGG/C/T JTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGGAAACACAAAGAGAAAAAAGG TTTATAGGTGGAGAAGAGGA
WI-18442	62 CT	---	---	TTGATGTTAATCTGCTACTCTGGAGATCGGCTAAAAAT/G/AJAAAGCATAGTTATTATTAGCTTTGG TATATCTGGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTTCCAACTCA
WI-18452	38 GA	---	---	ATATAAGCTGGAGACTGTGGAGGGTGAGAGCGAGTGGGACTAGCTGTTGAAAGAGAGAAATGTAGC AGTAGTAAAGATGAAGACTGCAAGGATTCAAAACA/A/CJGGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
WI-18489	102 AC	---	---	CTGGTGGGAGGAAACAAATTTGGGTATATTCATACAATGGAAGAACTCTTCAGAAATAAGAAAGGAA CAAACTGATGATCAACAACATGGACAAATCTCAATCATATTGCTGATGGAAAGAAACCATTC TAAGAATACACAGTACAT
EST5b	93 A	---	---	



EST5	93 A	---	---	---	CTGTGGGAGGAAACAAATTTGGTATATTACATAATGGAACCTCTTCAGAAATAAGAAAGGAA CAAACTGAAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGGAAGAAACCAATTCA TAAGAATACACAGTACAT
EST6	48 C	---	---	---	TTAGCTACTTTTTCAGAAATGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAGCTTTTCTTCTTTGCAACAAGACAAAGCAAGCCACATTTTGCATTAGACAGAT
EST8	158 A	---	---	---	GGACAGGACCTCTATTCCCGCTGTGCAGCAGCGGCTGATGGACTGAGCCAGGGGATCTGGGOC CTCTCTCAGGGCGTCCAGGACCCAGAGCTGTCTGCTTTGAGTTCCCTAGAGCTGTGCGGCCA GATAGCTGTCTGAGTTGCAAGCAGGATGGAGATTGGACACTGTGTGCTTTTGGTGGGT
WI- 18740c	104 G	T	---	---	TCCTCATTGTTGGGATGATGAGAAAGATGTTGGGAAAATTAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTACCATCATGTATC/GJAGTAGGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C	G	---	---	TCCTCATTGTTGGGATGATGAGAAAGATGTTGGGAAAATTAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTACCATCATGTATC/GJAGTAGGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C	T	---	---	CCAAAGTCTCTGCTCATAAAGAAATTTTGGGATGGAGAGAAATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCCTTCATTTTACAGAGGTAGCAAC/CJTTGATCCACAAACCCCTTCCCC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTGTTTCTCTT TGAAGCAATGACAAGCACTTTACTTTCACGGTGGTTTGTGTTTCTTAT
WI-18746	114 G	A	---	---	GCCAGAGCTGAAGTCTTTTCTCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTTACTTGACCGTTTTATATTACTTTTGTAATATCTTG/AJCCACATTTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112	212 G	A	---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCCTGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGTCTATCATGACAAACCAAGAAACCGACGACAAA TCTTTGCGAGATTTCTCTAGTGGCTTAGAACATGGCTTTAAGAAACACCGGTGATATCTTTGAG GGTGACAAGGC/GJCTCTTCAACAGTCCATACCACTGCTTTGCTCTAG
WI-19092	232 A	C	---	---	TGGTGGCTGGCTAGTGTCTTCTACAGAACATAATTTGCCTATAGAGGCTATCTTAGATCATGT CTCAATGGAACACACTTCTTCTTAGCCCTTACTTGAATCTTGCTATATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGTCTTTGTTATTAAGTGAATTTTC TTTTAAGCTAACAAAGATCATAAATTTT/CJATGATTAGCGGTGAAC
WI-19057	175 G	A	---	---	CCCAATTTATTAGGCCAGTGTCTCAAAGAGTAGAGGAGGTCTACTGGTCTTCACTCTTCA GTCTCTGACGGCGGACTTACCGTGACAGCGGAAGTGGTATGTAGTCCAGGACCGGAGCCACTG TCTTCATGCAGGAACACAGTGCAGATCCACAGCTC/GJCTCTTTCATCTTGGTTTGCCACA

WI-20103	168 C T ---	---	---	TGGGACTTCCAACTCAGAGGATGTGGGAATCCAGCTCAATGATACAGGATAAACTGGGATGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCCTGGGCTGGAAGCTGGGTCTCCCA[C/T]TTCATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGCTAGAGCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---	---	---	GCCTTACCCATTTGACATATACATATGCACACCTTTGAGTGGCAACATATATCCACACTA TAAACATACCACATTATAAATCTGTAAAGGACAAGAAATGG[A/G]TTGAATAAGTACCCCCCA CATATACAAGAAGTTAGCATACTTACCCGTTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ---	---	---	TGGTTACAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGCTTTTTAACTGAGTTAAAAAATAACAATGCAATTTTT[A/G]ACACTGTTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---	---	---	GTCTCAAGGGGGAGAAAACCTGGTTCTTTATGTACAAAGCACAGATGTAGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA[A/G]AAGGGAGTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156 A C ---	---	---	GTCTCAAGGGGGAGAAAACCTGGTTCTTTATGTACAAAGCACAGATGTAGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA[A/C]AGTTGGAAAAAAGGGAGTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47 A G ---	---	---	CAGTAAAGAGTGATTCAGTTGCAGTAATACACTGACAGGTAAATA[A/G]TATAACATTAGAAAA GCAAAATCTTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAAATGAAGGCAGTTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---	---	---	GCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAATGGAAGTGGTCATCAGGCAATA ATTGTTCCCTTGGAACTGCAACCGACTGTCCATGCTCTGTTGGGACTTACACATTCAAGTTTGACAG T/C]TGAAAAACCAAGTGGAGCTGCTTTCCAAAGATGTTCTGTCTTCAATAGGAATTCATG TTATTTCTTCTTGGCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49 G A ---	---	---	GAGTGCCATACCTTCTCCAGGCTCTGCCCCAAGAGCAGGAGGTGCCT[G/A]AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCACCTCCCATCCCGTAAGACCTCTTCCCTTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ---	---	---	AGCAGTGGCCTATTGCATCCAAACCAACGCTCTTGACAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTCCTACACAGTGCCTTTAAGTGAAAAATGGTCGAGAAAGAGGCAC[C/G]A]GGAAAGCCG TCCTGGCGCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTTGAATTTCTCAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTTCCTTTTGCCCTTTTGCAACC

WI-20146	31 T C ---	---	TGAGTCTTCTGTATTGAGCAGTTAGC[T/C]CATTGAGATAAAGTCAAAATGCCAAACACTAG CTCTGTATTATCCCCCATCACTACTGGTAAAGCCTCATTGTAATGTGTGAATTCATACAGGC
WI-18922	74 A ---	---	TAGGAATTGGTTTACGCGCTGAGGCAATTAGACACTTTTGAAGATGGCATAACCTGTCTCACCTGGAC TTAAGC[G/A]TCTGCTCTAATTCACAGTGCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCAGAG GAGCCACCAAGTTCTC
WI-18763b	53 A G ---	---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA[AGT]ATTAGAATG TACCATATTTTTTGTAAATTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCA TGTTTTTGCCAA
WI-18763a	38 A G ---	---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGA[AGT]GACGATGATGTGAATTTAGAATG TACCATATTTTTTGTAAATTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCA TGTTTTTGCCAA
WI-18771b	75 A ---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAAGATGTTGGG AACAGAA[G/A]AATAAAGTGAAGTTAAGGGGGAAGTTAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG[AG]AGATGTT GGGAACAGAAAGAAATAAAGTGAAGTTAAGGGGGAAGTTAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---	---	GGGAAAAATTTGAGACGCAATACCAATACCTAGGATTTGGTCTTGGTGTGTTGTATGAAATTTCTGAG GCC[T/C]TGAATTTAAATCTTTCAATTTGATGTTTCCCTTTTAGGTATATTGGCTAAGTGAAACTT GTCA
WI-18742b	51 C T ---	---	ACAAAGTCTGTAGCCCCCTCACCTTTCTGTTTTCACCTTTGCCAATGTAC[CT]ATCGGGTTTGGTTT TCTTGATATTAAACGGTTGTGGTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---	---	GTGTGTCCTCAAAATGGGGTCTGCTCTGCTACCTTGACCCCTTCCCTTCTCTGCTCTCTCTCATCA TCATTTCCCAACAACATCCTCTGCCA[CT]ACACAAACAAACGTAAGTTTCAATTTGGCAAAAAATTGA GC
WI-19970b	167 G A ---	---	TATAAGCCGAGTCAACGAGGAGCGCTGTCTGGCCACAGACAGGGGGTGCCTGTGGAGCCCTGCCACCC GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTCCAGTTCTCTCACTGCGGGGACCC AGCAAAAGGCTTCTCACTGGTTGGTCAAAAG[G/A]TAGTCACTTGGCCTGGTGCATCCACAGAGGA TGTTGTTCAAAACAGAAATCTTTTAAACGACTGACCTTCTTAAACAGA
WI-19970a	126 T C ---	---	TATAAGCCGAGTCAACGAGGAGCGCTGTCTGGCCACAGACAGGGGGTGCCTGTGGAGCCCTGCCACCC GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTCCAGTTCTCTCACTGCGGGG ACCAGAAAGGCTTCTCACTGGTTGGTCAAAAGGTAAGTCACTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAAAACAGAAATCTTTTAAACGACTGACCTTCTTAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTC ACATTCCTCTGCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTCAGTGGGTCTC TTGGGCTCTAGGCTCTGGAGATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAAAT/ G/ACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTC ACATTCCTCTGCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTCAGTGGGTCTC TTGGGCTCTAGGCTCTG/CJAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTC ACATTCCTCTGCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTCAGTGGGTCTC TTGGGCTCTAGGCTCTG/CJGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCC/C/GCTGGCTG TGCATATCCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTCAGTGGGT CTCTGGGCTCTAGGCTCTGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TTAATCCAGCCTACCTTGTAGTATTTTAGGAGACAGTCTCAAGCACTAAAAAGTGGCTAATTC AATTTATGGGTATAGTGGCCAAATAGCACATCTCCACGTTAAAGACAGTGGATCATGAAAGT GCTGTTTGTCTTTGAGAAAGAAATATGTTGAGCGCAGAGTAAATAGGCTCCTTCATGTGGC GTATTGGCCATAGCCTATAATTGGTAGAACCTCTATTTAAT/CJTG
WI-18944	147 A G ---	---	CAAGGCCAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAACAAA AATGCCAGAGGATAATATTGATCTCCACATCTTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC/CJGTTTAAATTAATTCACAATATAAAGTTCTACAGTTAATTTATGTGCATA TTAAACAATGGCCTGGTTCAATTTCTTCTTCTTAAATAATTTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTCTGTAATTACAACATAATATTATGCCCTCTCTCAGACAGTCAAAAGGAACTGGGTGGT TTTTGTTGCTTTTATAGATTTATGTCCTCATGTGGGATGAGTTTTTAATGCCACAAGACATAATTTA AAATAAATAACCTTTGGGAAAGGTGTAA/CJACAGTAGCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGTAGCTCACGAAACTGGAATAGCCTTCGAAAAGAAATGTCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTGTGCTGATTTGACCTGTATTCAAGTTAACTGTCCC CTTGGTATTGTTAATACCTGTACATATCTTTGAGTTCA/CJCTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAGAACGTGCTTGTGGAAAGACAACTGTGTGGCTTG

WI-19042	193 A C ---	---	---	TTTGTAGTGTGCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGCCACAGAAGGTGAACCTTTGTGCTTCAAGGACATGGTGAGAGTCCAACAG ACACAATTTATCTACTGCGACAGAACTTCAGCATTTGTAATATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGTATTAACATATCTCTTTGGACTTCTGAAGAGACCACTCAAT
WI-18984	208 A C ---	---	---	ATTGGCCCTGTACAGTTTGCATTATATAAATTCATTAAAACACTACAGGTGTTGAATGGTTAAAA TGTAGGCTCCAGTTCAATTTTCAGTTATTTCTGAGTGTGAGACAGCTATTTCGCACGTATTAAT GTAACCTATTAAATGAATCAGAAGCAGTAGACAGATGTTGGTCAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAAATGCTAAATGCTAAATTAATCACTGGCATGTTGACT
WI-18851	90 T A ---	---	---	GCTTCAATTGGCGATTGATTGAGTGCCTCAATGTAACAGGTTGGTAGTTGTTACTCATTTTGAAT ATACCTTTTCTTATTGTTATCTT[A/G]TAATATAGGATCCTGGAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGCTGGAATCTGTAGGAGCCCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCAATGCCCCGGGGGAAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGCTGGAATCTGTAGGAGCCCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCAATGCCCCGGGGGAAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	---	ACTCCTCTGCTGCTGCCAT[C/G]ACTGTCTCTTTGAACCAGGAAAGTCACAGAGTTTAAAGAGAA GCAATTAACATCTGAAATCGGGAACAAGGGTTTATCTATAAAGTGTCTCTCCATCACGTTG CTACCTTACCACACTTCCCTCTGATTTCGCTGAGGAGCTGGCATCTCTACGTACGTGGCATAAC ACATGCTGTAGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---	---	---	TGGAAATTCCTTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAGGGTCAGTA TGG[G/C]TAGGGAAACATTCCATCCTTGAGTCAAAAATCTCAATTCCTCCATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	---	CACGGTCTCTGCATGTTACCAGAGCGCTTCTGCTCTAGCCAGCCCTGTATGACCCGCAATA TCCCAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---	---	---	CACGGTCTCTGCATGTTACCAGAGCGCTTCTGCTCTAGCCAGC[A/C]CCTGTATGACCGCGCAA ATATCCCCAAAGCTTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---	---	---	TTGAGGAGGTGGGGTGAACCTGCTCTTGGCAGGGATTTGTACACTGCATTGCTGGGCTGTTCCTT/ CJGGGCTCTTCTGGACCTTGACCCGTGGATACCAGGCCATGTGCCATGTTATTTGGGTCTCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	AGGCGTGTGGCTTATGTACCCAAACAGAGGGGTCTGTGAGAAGTCTGGCTGGCTGGGATGGCCCCCTGCC CCCTCCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAGAGTCTGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTGAACACCTGAGGCTTCCTGTGGCCACCAGGCACCTACGGCTTCCTCTCC AGATGTGCTTTGGCTGAGCACAGACAGTCAGCATGGATGCTCTTGGCCA
WI-19016b	184 C A ---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCAGTCTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAAATTTTGTATGTATTAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAACACCTTAGATACATAGCCGACTGTATACAGAGGTTATCTCAAC/AJCTCAACACTATTGAC TTTTGGGCTGGATGTTCTCTGTGTGGGGTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCAGTCTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAAATTTTGTATGTATTAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAACACCTTAGATACATAGCCGACTGTATACAGAGGTTATCTCAACCTCAACACTATTGAC TTTTGGGCTGGATGTTCTCTGTGTGGGGTTGTCTGTGCACTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCATTATTTCTTCTGTGTAGAGACTGGCACAAGCTTTGGCTAAGGACACCCGCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAACCCAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAAAGCAGTTACTTTATTTGAACAAGGAAGTGGCATAGCAACTCAGTGTGCC CTTAGGTGGGAGCTCTCCGCACTACCACCTCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGTAGCTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAACCCAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGC CATGAGTATAAGATTAAAGCAGTTACTTTATTTGAACAAGGAAGTGGCATAGCAACTCAGTGTG GCCCTTAGGTGGGAGCTCTCCCACTCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGTAGCTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCCAGCTCTGTATCTGTCTGAGGGTTCTGTTCACGGCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAAGGCCAAAAGAACATACAGCCCAAGCTCTTAGAGGCTCCA[GAT]CAGAA CTGGACCTTTAACTACAAGGAATCTTGGATGAATTTTTCAGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGACACTAGGCCATCTTCTCCCAATGTCCTCCCGGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCTTGCCCTTGACGCCCATTCAGAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTTGCTGACATCTGCCCTTATCCTGTCTCTCT CCCCAGTGTGTACACTTGGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGTAGAAC GGAAGGAAGGGGGGTCTAT[G]AGGGTATGGCTCTGTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAAGGAGGTTTAAATGAATACCTTTGTTTGTGTCATGTTCAAAAAGAGATTAAT ATTTTGTAGCTGCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTAGGTTAATAATAA GGCTATTGTCCACCCACTCTTCGGCATTTGCTGGAATATCTGGGCTCAAGTGGGAGGCCACGTG GGAACAAGGCTCAGAAAACAAGGACATGCAGCTCCCTGAGCCAGTTCT

WI-19766b	93 A G ---				TGGCCTCAATGACTGGTACATTGGAGAAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAGTC/A/GJGACAAACAGAAAGGACACACCAAGCCTGAAACCCCTC CGGACACAGGAGAGTTACAGCTGAGGATGTCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---				TGGCCTCAATGACTGGTACATTGGAGAAAGCTG/AJTGACAGCAGCATCCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAAAGGACACCAAGCCTGAAACCCCTC CGGACACAGGAGAGTTACAGCTGAGGATGTCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---				CTTCCTCTGTTGGCTTGCATTGTGCGATTGGAAACCAACCTTGGAAAGGGACTTCTCTGCAA AACCTTAAAGACTGGTTAAATTACAGGGCTAGGAAGTCAGTGGAGCCCTTGAICTGAIC/GJAAAGC TTAGAAAGGAACCTGAATTGCTTCTTGAATATGGAATTTAGGGCGGGCGTGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---				CTTCCTCTGTTGGCTTGCATTGTGCGATTGGAAACCAACCTTGGAAAGGGACTT/GJTCCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCTAGGAAGTCAGTGGAGCCCTTGAICTGACAAAGC TTAGAAAGGAACCTGAATTGCTTCTTGAATATGGAATTTAGGGCGGGCGTGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---				GGGCTTAAATCCCTCTGTTGGGACTGGTCTCTCCAGTTACAGCAAGGATCGCACCCCTTTTCC ATAACCCCTTCTACATTGGAAGAGCAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAATCACAGCTAACAAACGATGATGGCTCACAGTAACCAACACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---				TGTTGAAATAAAATTTCCATGGTCTTAAATGAACTGTATGTTACTTCTTTTAGAATATCCTTTT TTCATTAAATAAT/CJCTAAACCACTATGTGTTCAACCTTCTGTTTAAACACTAAGATATGGGT TTTTGGAAGGCCACAAAGTCACAGCTCCATGAAGTGGGCGAAATGGTCTTGTTTGGAAAGCTCTC CAGGGTGTCTCCAGAA
WI-19909a	29 T C ---				CCAGAAATAAGCCTGAATATCTCTT/CJTJTAATAATAATTTTCTCTCTTGGCTCTCCAA GTAAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTAACACTACCTAGGCGGG TTTTTCTCTTATACCTTGTTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---				TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTGCTTAGGGGCATGAGACATTAGGAAG GCCACAAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCATTTGTTAGCAGGA GGCAGGAAAGTATCTGGGCTCTGCGCAGCAAAAGCGTGGTAAATATTTGGGTGACGTCATGC ATCCCCCATGCATTGGTTTTC/CJATGTCTCCAGTGAGCTGTGGCAAGTCT

WI-20113	60 T C ---	---	TTCTGGTACATGGTAAAGTGCTCAGTATTACTAGTGAATGAGCAAGACCTGAAATACTGTC/GGGA AACAGTAAAGCAAATTACCAACAAATTAGGAGGAATTATTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAAATTCATTCCATAAACAGGAGGATGAATAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107 G C ---	---	TGATGGCAAAGTACAAAGGCTCTGAAGAACAGAGTAACAAGACAGCGCAGTGCAGCGTGTGGC CACTCCACAGGAGCAACACTGACTTCATTAGGCAAA/GC/TCTTACTCTGTTACTTTTTCCTC CCACATAGTTTAAACCAATAGAAAGGCATTCTATCTCACACTACTGCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAACAGATGCA
WI-20721	72 T C ---	---	CCTGCAATCACAAAAGTGGAAGTGTGATATTTTGAATCATACTTGTATTTAACCACTTCAGAAA TTCTAT/G/AAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 A G ---	---	CTGGATTTTAATTTCTGGCCTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTGGCAAGATCCCTAAGTAAGGTATTGACGACTGAGACTAGTCGGGCAAA GTCATGAGACCCCTAGCTGATCTCAT/G/AGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 C T ---	---	GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GGGTGCGATGAAGAGACTGTTGGTCTATGGCGGTGA/C/TGCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGTTGTAGAAAGTCTCC
WI-19348b	98 G A ---	---	GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GGGTGCGATGAAGAGACTGTTGGTCTATGGC/G/AGTGACGTCCTTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGTTGTAGAAAGTCTCC
WI-19635	98 A T ---	---	ATTAGTTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACACAATG TTAAAGGTACAGTAAATAACAGTATTAT/G/ATCTTATTGTAGCACGGCTGTGAGGCTCATTT GTTGAATGAAGCATCCTTAGGCAGCACGTCGACTGCATGCAGATATGTGTGCTGAAGAAGACTTTGCGCTT T
WI-19641a	46 A G ---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG/G/TATTATAGTCTCATGTTT TTAATTTATGAATAACGTCGTGATTCATTGATTTTGTATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAAATAAGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAAATGAGGTAGTATTTTAAATTTTAAATTCACCCACCTG
WI-19642b	52 C A ---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCTGGACACATTATCCCCCTC/A/GGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTGTAGTGACACAAGTTTTCATGCTATTA
WI-19673b	180 C T ---	---	TCTGCCATGATCAGATTGTGATGAMGACATGATGGTCACTAGTAGGTAACCTTCTGTGTCTATTGCGCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCAGCTGTAATCTAATAGT GAAAGGCCAATGATGTCTCAGTATCACTGTGAAACATTTTCTGCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACAGTCAAAAAACACAGCCC



WI-19673a	35	GA	---			TCTGCCATGATCACATTGTGATGAAGAACATGATG[A]TCACTAGTAGGTAACCTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGATCACCACCTGTAATCTAAT AGTGAAAAGGCAATGATGCTCAGTATCACTGTGAAACATTTTCCCTTGGACCACTGTAAGAA TCTTGAGGAGCCTGAAGGCTCAAGGTCCACACGCTCAAAAAACACAGGCG
WI-19724	35	AG	---			TTTATTGGGAAACAAAGGATTGTAATTTGGTAA[A]GCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAGCAACACAGAGATTTGGTTTTCTCTT
WI-19307	196	TC	---			TCCTCCTCCCCAACTAGATGGTATTGATCCTCTGCCCCACAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGAATTCCTTATGAGAAATGGTGGCTTGGGATGGAGGTGACATCCCTTCTGT GGTGAATCTGCAAGAAAGAAACCAAGCAATGTATTCATAGAGCCCTTAAAGAGACCCGTCJTG AAATGGCCCATGGTCTAATTTGGTGTGAATAAATAACCTCTTTGGCTG
WI-19269	85	AT	---			CTTCCCTCATCCCTCTCCACCACACCATCCCGGAACAAGTCTCCAGGATTCCTGCCACTGGC CATTTGGAGTGTCC[A]TTGGTAGCAATGTGAAACCAACAGGGCCTTTGTGGAGAAAATGG AGGGGTGAGGGAGTCCAGGAGGGCTTATTGAGGGCTTTGCCACTTGTCTCATAGGCGAGCTCG ATCTCCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGGTAGGCA
WI-19946	122	CT	---			CAATGGACTGAATGAGTGCCTGGTGGGGGGGACACACACCTTCAATACACGTCGAAGGTGG CTTCCAGTTTTAGAAAACAGAAATCTCATCTCAGCTGAGCGACAGAGAGGT[C]TTCTTCCCTG ACCCAGAGCACTCAGAGCCAGGCTCTGGTTTTTCAAACTGCATTTAACCTGGCCAGAGAGTTAC CGTAGGCATCTTTAATAAATACTCACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	GA	---			CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTTTAATGCAACCATAAATAATTATA ATAAATATACATCAAGTAACCTTACAGCACATTTTTAGGGCCAAAGTTTGGATCTGTCTGGACCT CAATGT[G]AICTCTCGGAGAACGACCCAGCTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCCAACAGAGCTTCTGAACCTCCTCTGGGAGGTAGCTGACMAG
WI-19076	40	GA	---			TTGGTTGGTACTTGTCTGGAAAAAAGCAGTTTTAA[G]GTATTCAAAATACCTTTTAAAAA GTATCTAGCACAAAGATTTTCTGTAACTAGATTATGTTGAACTTTTCTAAATCTTTGAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCCATCCAAATCTATCTGGCTCCTGAAAAACTGCAGA AAGGCATTTGAAAGCTGTTCTTTAAGATAAGGATTTCTTTTATCTT
WI-20218	26	TC	---			CCACACACTCTGGTTTTATAAGCTA[C]AGGACAGAGCAGATGGAACCTGAAAAACAGGGTAG AAATAACATAAATGGAGGGGAACAGTGGGATGCAGAAAGAAATGACAACAGCCACATGTGCCCA GTCAATACTTTTAGTCCCTGCAGCAGAGATGCCAACCAAGTCTCTATACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	TG	---			CAACCTTTTGGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATCATAATTG GGAAITCCTCTTTTAAATATCTCCAGGCTTGATTGGGAGGGGCTGGCTTACCCCTTCTCTTCCCA TCCAGTCTATTGCCAGAT/GPCCAGAGAAAGCGGGGAAGCCCAAGCTCTCCAGCATAGCCACTGTGG GTGGGCTTCACTTCTGTCCAGTCTCTGCTGGGACTTGTCTTTCGGGG

WI-20361a	192	GA ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAATATGTGAATCTGATGTCAGAGATTACACTCTGCACCTCCAAGCTA CAACAGTGCACAGCTGAGAGTTTCCCTATACCTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTC AAATGGGAAATTCCTAACTACACGAGACAAATGGGTCTCTACAGTAGGCCCCG
	75	AG ---	---	GAGCCAAACCCAAACAAATAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT TCAGAAATT[GT]CATAAACATCATCTTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTCA AATTCATCTTTCTCAAAATTTAAATTTGTTTAAATCCCAAAGGTCCTATTGAATCTTCAAAAATA AACTGCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20572	133	GA ---	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAAATTATAAGTTGAATAAATAGTATACAGCAATC TTCACCTTTTAAAGAAATGTGAGATCCTTTGTTGGTTTTTATTTCCTTAAGTACAAAATGCTAAAC[ G/A]GGAGCCGAGCTCTCCGCATTCAGG
	79	AG ---	---	TGACCTCATCTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTG CTGTACTTCAG[AG/TTTAAATCTGGGAATGAGCATGACGAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGAGTGCCAGGCTTCAOCAGACTAT CCAGAAAGCATTCATGGGGTATTGGTCTGCATACGTGAGACACTGAGCT
WI-19765	57	TC ---	---	TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGATACCTTGTCTCTCA/T[C/JATGTATCT TGTCCTGCTGCTTTTAGGTAGCAAGGTGATGAATCTTTTAAGTTTGTGTTCTTTTCTCTCGT GGTATCAGTGAATACTGATCTATTCTCTGGCTAGGTCAATTTACAAAATTGCCATGGAACTGAGC AAAGGCCACGTGGGATAAAATCACTACCATCGACGCCACCAGTATT
	239	AG ---	---	TGACAAGGGAGAGAGGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTGCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGCTGGTACCCCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTACAGT ACCATTCAGGCAAACTTTTCTTAAACGCTTCAC[T/A/G]GTTCTTTTAA
WI-19066g	184	CT ---	---	TGACAAGGGAGAGAGGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTGCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGCTGGTACCCCTGTAGCTGAATTAATCTCTCCATATTC/TGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCTTCACAGTTCCTTTTAA
	148	TC ---	---	TGACAAGGGAGAGAGGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTGCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGCTGGTACCCCTGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCTTCACAGTTCCTTTTAA

WI-19066e	147 GC ---	---	TGACAGGGAGAGAGGGAATCTACTATTGCAAGGAAATCCTCATTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACCTGG CATATGTTCTTGGC[G/C]TTGGTCAACCTGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066c	100 GA ---	---	TGACAGGGAGAGAGGGAATCTACTATTGCAAGGAAATCCTCATTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAAC TGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066b	87 CT ---	---	TGACAGGGAGAGAGGGAATCTACTATTGCAAGGAAATCCTCATTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAAC TGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066a	72 CT ---	---	TGACAGGGAGAGAGGGAATCTACTATTGCAAGGAAATCCTCATTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAAC TGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-20660	105 GC ---	---	TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAATGTG TGCTAAATAAATCTCCCTTTTGAATGATATTTGT[G/C]TTAATAAGGGAAGCATTAAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATTCCATTACTGTTTCTGTACAAGATAGAACAA AAGCTATCCACCCGCCCCCAAAAATACTGTTTAAACAACACTAGTTTAAAGA
WI-18768	120 CT ---	---	CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCCCTCCCTCAGTCTTCC TCCACCCGCTCTTCTTCCAGCCTGCCTGCATGCTGCACCCCTTGGT[C/T]TCGCTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37 AG ---	---	TTCCCGAGGGTCTGTATTGCAGCTAAGCTCAATGT[G/T]ATTAACTTCTAGTTGCTTGTCTTTG GTCCTTCTCCAATGATGCTTACTACAGAAAGCAATCAGACACAAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGCAACCTGTAAGTCCCTTTTAAATGGCATGACAAAGGTGTGC AGTGGCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-18790	49 AT ---	---	GAAAGCCAGAGATTAGCCCGCATTCGCGATCTGTCAACCAAGGACAGAAATGCGATGGACAAGGA TGAGCTTTACAAAGATGATGACCTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTGGGAATGCGCT
WI-18987	35 GA ---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTC[G/A]GTGGCCAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCCTGCTAGGCTGGACACAGGATTCAGAAAGACACCCAGGCTGCACA GAAAGCCAGATGGACCTGAGTGTGCGTGCAGCCCTTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA

WI-18919	26 C T ---			TGGATGAAACACACAGGGATTCCGGAC/TJGCCAGACCCCAATTTTACTTCACCTTTCTCTACAGTG TTGTTTGTGTTGTTGTTTATTTTATACCTTTGGCCATACACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI- 18741c	64 G A ---			CTTCTGTCGAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI- 18741b	38 G C ---			CTTCTGTCGAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTOG CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI- 18741a	23 T G ---			CTTCTGTCGAAGGCTTTGGACAT/TGJCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTOG CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI- 19179a	170 G A ---			TCAGAAGCAGACATGGCATCTGTTCTCTGCTTGTGTTGTTGTGTAOCTTTCACGAGACCTGAATT TTAGAAATGCCAGTGTGCGCAGAGTGAGTGAGTGAATTTCTCCTTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTTCATAAACATATCAACC[A/GA]TAGCATTAAOCCATTTTATTCCTGTCCCT AGTGTCTGAAGATGCTCACCAAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	48 T A ---			CCAGTTGCATCCATGTTTGAATTTCTGATGAGACTAGAGTGACAGT[A/G]TTTCAGAACCCAAATGT CCTCAGGTAGTTTGGACATCTCTATGAGATGGGATATGCAGATGGCTATGGAAATGCAGCTGC ATAATTACACATTATCAAGTCTCTTACAATTTATTTCCGACGATGTAGCTAAGTAGACCCA ATGGGAGAGAAAATGCCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G C ---			CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAGCACACATTGGATG GCAGCATGGGTTCTTCCCATTTATGGGCATGAAATATGGTTTAGAATAAGGAACAAGCATTATT CCTTGGCAACAGCCTCACTAAGAGGCTTTTGTGCTGAGTCAAGCAAACTTGGCTGCTCTGCC CTTGGAG[G/C]TGCAATTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI- 20014b	214 T C ---			TTGAAATCCAGTCTCTGGCCCCCAGGCGGTCTGTACCATAGATGTCTTCTCTACTGGGTG GTTCTGGCTTTTGTAGAACTTGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAGAGCAATGTTCTTGTATTCTGAACTGGAACCTGAACAGTTTGGCTTTCTCCTAGTCACC AAGCATACTT[C]TCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C ---			GTCTCCACAGAGTCTCTGCACCCCCAGCCCTGTCTGCTGTAAAGGGATACAGAGAAGCTCCCG TCTCTGCATCCCTTCCAGGGGGTGGCTTAGTTTGGACATGCTGGTAGCAGGACTCCAGGGCGTG CACGGTAGCAGATGAGGCCCAAGCTCATCACACAGGGGGCCATCCTTCTCAATACAGCQ[T/C]G CCCTTGCAGTCCCTATTTCAAAATAAAATTAGTGTGCTTGGCTGTCTGT
WI-19135	20 G A ---			CAGTTACCTGCTTGGCTC[G/A]AAAGTGTCACTAAATTTGTAATTTTAGTATTAACCTCTGTAAAGT GTCTGTAGGTACGTTTATATTATTAAGGACAGACCAAAATCAOCTATCAAGGCTTCAAAAACCT TTGGAAAGGGTGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAACCT GCTTTTGGCCATATAAATGCTGATATTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54	G A ---	---	TACACAGAGGGTGCACCTTGGACTCTGAGGGTTGGGTGTGGAGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTGACCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGAGGT CACCTTACCCCTTTTCATAGGGGAAGAGTGTACACACTCCTGGCTATCTCAGGGGGAATGGGAAAG AATCTTCAAGGGCAAGAACTCGTGGAGGATGCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTCCAGTCTCCAGAAAGCAAGGACTGCCCTTCATTCAGCCTTCTGACCTCCAGCCTTCTAAGG CTAGCCACACGGGACTCTGGTGGCTGCCAGCTTGTAGCTATCTATATTCATTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGAGGCTGTAGCCAGGAACCCCTCTCTTCCCTGGT CTGGCTCTGCTGGAGCG[G/C]TGGGAACCAACACCTTCAGTGTCTGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGGTGGCAGACAACACTAG[C/A]ATTTACCGGGTGTGGGCAC ATGGGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA C/TGGCAGATGCCCTGACAGAGAGTGGGTGGCAGACAACACTAGCATTTTACCGGGTGTGGGCAC ATGGGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAAGACCTAAACATGAAGGAAAGGGTGCCT CATCCAGGAACCTGTCTTGTGGGTGATGATCAGTGTGCTGTGT/CJGGCTCATGGCAGAGCATT CAGTCCACGGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTCTGCTGCTCAGCTCTCCTGCTGTGATGTGGAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTCCTTCACTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCTTGCCTAATGTTTCAACAATGGTGGAA[G/C]GCTTCATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCAGCACTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTCACCCAGTTTAGTTTGGGATGATTTGATTTCTGTGTGTTGATCCCATTTCTAA CTTGGAAATTGTAGCCCTCTATGTTTCTGTAGGTGAGTGTGTGGGTTTTTCCCCACCAGGAAGT GGCAGCATCCCTCTTCCCTTAAAGGACTCTGCGGAAC[C/T]TTTACACACCTCTTCTCAGGGAC GGGCAGGTGTGTGTGTGTTACACTGACGTGTCCAGAGCAGCACTT
WI-19117	134	A G ---	---	AAATAATGCAACGAGGAGGAGAAAGAAATGCACCTAAGACAAGAACATTCTCTCATAGAACATTG ATCTGTTTACAGGAACAACACCTTGCCTTGAATTTACACAGTGAAGTGTACATAATTGCATGAA A/GJTAGCTATTTTTCCTAAGACATTTTTCATTCATGAATATTTTCAAGTTTTTTCATACTGTACA CATTTCTTAAACACATGATACCGACGAACTGAAATGAATGCCGAATTTG

WI-19134c	263	CT	---			CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTACACACTCTGTCTCCTCTATCTCCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCCATCCOCAGCAAGGGGTGCAGCCAGGGTCTAG GCCCTTCAGAGCCAGGGCTAGAGGATGACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAGCAC TTATCCACTTGCTCCTCCTCTACCCTCGGCACCCCTGGGTGGAAAGGG
WI-19134a	162	TC	---			CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTACACACTCTGTCTCCTCTATCTCCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCCATCCOCAGCAAGGGGTGCAGCCAGGGTCTAG GCCCTTCAGAGCCAGGGCTAGAGGATGACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAG CACTTCATCCACTTGCTCCTCCTCTACCCTCGGCACCCCTGGGTGGAA
WI-19224	112	CT	---			GGTTTACCAGTCTTCCAGGGAATCCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGAGATTAGATCCAGGAGATACACAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTCATAATCCAGCAGGCCAGAGACTTCC AGGAAACTCATTCAAGGAGGTGAAATGATGATGACTCTCCAAAGATGAAAA
WI-19201	179	TC	---			GCAGCTCCTAAGGACCCTGGCCATTAGCTCTTGCTTTTGATGGCATCTCTTCCACCTTGCTTCTC CTTTGCTCCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCGCCCCCCACACTTTGCCCTGCAGGTGCACCGAAAGGACTCTGTTGGGGGATAAAATTCAAAAA GTGTGATGTGCTGCTCAGAGGTGACACTCCATGCTGCTGGCTTGGCTCAA
WI-19034	45	TC	---			GAAATGGTCCACTCAGAGCTACCCCGGTGATGAGGATGGGAAATCTACTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTTGAAGTGCATATAAATTTTTTG CTAGCCCATGATCAATCGACTCTATTGTTTGATATACACTTCAGCATTTAAGTCTGTGCGAATTGAC ATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGCTATATA
WI-19102	25	CG	---			TGTTCTGAGTCACGCTGAGGAGAGCTGCTTCACTCAGGAGTTTCTGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCTTTGGAAACAGAAATGAAGCAGAGGAACTCTTAATCTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAAGTCTAGAACTCCTGTAAGTTTTGAACTCAAGGGGAGAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTGCGAGTCCCATAGAACAGAAATGGG
WI-18548b	65	AG	---			AAAGGAGGGGAGAAATCTTTTACATAAAATGCCCTTGATCATCTCCAGTCCCTCCTCACTGGGGAA[A GJAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	GA	---			AAAGGAGGGGAGAAATCTTTTACATAAAATGCCCTTGATCATCTCCAGTCCCTCCTCACTGGGG[G/A]A AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	TC	---			GGCAGCAGCTTTTTTAATTTGAACACTTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTTTGAAGTCCACAATTTGCAAGGCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121	CT	---			CAGAGGGAAGATTTATTGAGTCAGCCACAGAGAACAGAGAACACAGACACAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCTGCGAGGACAGAGGGGCGCTTGGACAGCA GCGCATGCCACAAACATTCA

WI-18017	87	C A	---			ACAAAAGAAAATGGAAATAGTTTGGGAAACCTTATCTGCATGTACAAAGTAATCCCGGTAGATAA GGAGAGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATAAATATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101	A G	---			TTATTGGTTCCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTCAGAAACCNCTCGATTCTGAATATCCC[A/G]TGGCGGCATATGCAAGGAAGATGA
WI-18254	64	T C	---			TATACGGATCATGTATTTGTGTGACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCACAT/C ]GCCAAATCCCTCTTCTCTTGTAGTCACTCTCTCCAAACCCAGGNACTTGGCAACCTGTTT TCCGTTCCTAGACATTT
WI-18265b	117	C A	---			CAAAATGGGTGGAGTGAGTATAAACGCATATTGAGAACAAAGACGGCCTTCTGGCCNCTCTCGGTCC AAGGCTGTAAAGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTGGGTGGTTCCTCAG
WI-18295	40	C T	---			ACCACACATTTGTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAGGTTGATTACT TCTCTCCAAAGGATGATGTTTAAATGAATCCCTTNCCTTAGCTTCATCTTCATAATGCCAA
WI-18459b	64	T C	---			GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ C]GAGTAATTAACAACATAATATTTANATGACAGTGAATTAATAACGCTCTGGGTAAGCCAGAG GGGAGAGGGGGCTTTCA
WI-22585	56	A G	---			TTATTTTAAATTTGCATCTGAGATAATAAAATTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGGAGGTATCCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A G	---			GGGCTGTGGAGTAACAGAACTTGATGGAAAAATGGC[A/G]TCTGTGTAGAAATGATCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---			GCCTTGTCTTTGTCTCAGAGGCTCAGATGGATACGCAGCACTTCTTTTGAACCTTTTAT TTTCTGGCAGGAAGA[A/G]GGATCCAGCAGTGAGATCAGGAGGTTCTGTGTGCACAGACAG GGAACAGGC
WI-19888a	98	C T	---			GGCAGGATTCACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTTGATATGATG AAAATATTTGGAACTAGAAAGTAGCAGTGA[C/T]GGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCAATTTAAATGGTAAATTCATGTTATGTATTTACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATTACATGAGANCAITATTATGTTGGAAGTGAACACAAG
WI-21485	82	C T	---			TGAGACCATCCTCCTCAACAAAGAATCAGTCAGTTCAGCACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]T]GTGCACACAGTACAGTGCACAAATCCAGAGGGCAACAGATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---			TCAGAAATGCTTTCCACTGCCCCAAACCAAGAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCTCTGGAGGTGCATGACAGGATTAGTCTTCTGTGTTT/C]CTTGGT GCAAGTTGAACCAAGTGAATATGTACCAATTCATCAGAGCATCTGTTCCCTGTCCAGATCCCACTAG

WI-20561b	94 T C ---	---	CGTTGCTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGGCATTATTG TACTTCAGATGAAAAATCCTTACATGTCG/GGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25 A G ---	---	CGTTGCTATTAAAGATGGCTGTTTAAAGTATAAAGCAGTTTGAGCAACACTGATTGGCATTAA TTGACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69 T A ---	---	GCCTTCATTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCCTTCAATATATGGCGTTAGAAT AT/ATAAATCTATATCATATATTTATACACACAAACACATTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCCTCTCCCATGCCACTTAAATGNGCACAGGTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116c	59 T A ---	---	GCCTTCATTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCCTTCAATATATGGCGTT/ATAGAA CATATATAATCTATATCATATATTTATACACAAACACATTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCCTCTCCCATGCCACTTAAATGNGCACAGGTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116a	22 C G ---	---	GCCTTCATTTCTGTCAACCCAC/C/GCTGTCCACCAGTTATGTTGGCCCTTCAATATATGGCGTTAGAA CATATATAATCTATATCATATATTTATACACAAACACATTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCCTCTCCCATGCCACTTAAATGNGCACAGGTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133 G A ---	---	AAAGATTGCAGTCTGGGACACAGTTTGGAAACACTATTTATAAGTTGACATATTAACAACAG NTCCCAATGGTGAACCTGGTATTTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC G/ATGTGAACATAATGTTTAAAGATTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTATCCCTTTTCAGGTTGAT
WI-21444	39 A G ---	---	CTGGGACGCAAGTAACCAATTTAAAGAACTACTCTCAAC/GIAGTCTTTTTTATGGGGTATTTCA GTTGTTAAACAAAGTTAAATACTTATTGGAACATACTTTGTTATTTATTCGAGGAAGAATACT ATAAGATTGACTTACTACTATTGTTGACTGGTTTTTGAAGCCTTACTGGG
WI-21034b	148 T C ---	---	AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGATGAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAACTACTGGTCATGG GAGATTGGATAGAT/C/GCCTAACCTATCTCAATTTAAGTAATGTGAGCAA
WI-22091c	205 G A ---	---	GGCGTGATTTGATGCAATGTCCCAACCAAGTCAAGCTATCATTTGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCATGTAACATACAAAGCATATTACCTCCCCCTTAAGTGACTCATAATTTTC ATTACTGTGCTGTAGCTTTTAAAGGTTTAAATGTTAGGATTAAGTGGTATTACTTGAAGGCA ACA/G/ATAATTACGGCTTAACAACACACTAAATCATGAGGCTCAGGGATTG



WI- 21805a	45 A T ---			CAACTGCTCTGAGGCTCTTCACTAGCTGATTTATAATCCTATATTAT/AAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACTCTCAAGGGTGGATATGTTGGATGCAGACTCCATCAATATGTGTGGTT TTGTTTGTCTTTTGTAGCTTAAGTCTGTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTGAAGGCTGTTTGTAAATGCTG
WI- 21778b	155 T C ---			AAAAATCCATAATATTGAACCCCAAGTTACAGAGAAAGTTCGTAACTTTTTATTGAATTATTGAC TCTGCCCGGTGTGTTGGTGGCTTCAACTCCAGTCTGTAATGCCCTGTGTAGTGGGTGCCAG GTCTGGGCTTCTGAGGTCTGCTGGTAGAAGGAGGGCAGGTGGT
WI-20907	241 A C ---			TGAGTCAGTGGTCAGATGGGGCAGTTGGCTCAGCTGCAGTCCCTGACTCCGGAACACTGTGCCTCT CAAATGATCTAGAGCTCATCTTGGGGGTACATGAGGGCAGTTGTTCTAGTACCCATTAGCCG ATGGCTCTTCAAGCCAATTACACTGGGAAACACACCCCTCACAGATGCCTATCCATTTGAGTTG ATACAGGTTTTAGTAGCTAGAACTAAAAACATTTTAA/CJAATTATCTA
WI- 21449b	222 C T ---			AACAGCAGCAGTCACITCCAAAATGCAAAAAAATTACAATTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAGAAGANTTGAAGGTACAAGAAATCAATCAAGCAGCACTGGAGGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAAGCTGACAGAAAGTCCCACTGAGAGGCTCCACACCC AAATCATACCCCTCAGCTTCCCA/C/TTGACAGAGCCAGTCTCTCTGGGTTAG
WI- 21558a	157 G A ---			GCCTACAAGGAAGCCTGTGGACAGGCGAGNTGGGTGGAACCACTCCAGCTGGAACCTGOCCTC CCATCCCCCTTAGCGCTCTTGGCTTCCGGCTGATTTCTTGACAGCAGTCTGCGCAGGGCAAGG AGCTGTGGTGGGGGGCAGTATG/AAGCCAGGGACTCCCTCCACAGATGAGGCCTAGGGCTGCAA AAGGGCCCCGTGAAGAGAGATGTGGTCAAGGCTTATGGGTCTCTCCACC
WI- 22187b	178 G A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCGTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAACCAAA/C/A/CAAAACAAAACAAAATACCA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/A/AAATTCATGAAAATTTCC CCTAAACCATAAACAAAACGTCTCTCTTACCCCAAAAGTCTGGAGGAAAG
WI- 22187a	110 C A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCGTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAACCAAA/C/A/CAAAACAAAACAAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTTTCATGAAAATTTCC CCTAAACCATAAACAAAACGTCTCTCTTACCCCAAAAGTCTGGAGGAAAG
WI- 21809b	146 G A ---			TCATGAATATGAGCCTCCATAATCTCTCCCTTGTAAACAAACGTGCAGTCCGTTCAAGCTGTAA AACAGCCCAACCCAAAGACATCAAGAGGCAAGAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTCAAAG/GA/AGGGTCCCGGTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 CT ---	---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACAAC/CTGTGCAGTCCGTTTCAACAGCTGT AAAAACAAGCCCAACCCAAAGACATCAAGAGGCAAGAGCAGTGGCAGTGAAGAGGAGCCTGTGA AAGGATGTTCAAGGAGGGTCCCGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGAAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 TG ---	---	---	ACATTCGAGCCAGTCTTTCCATATTCCTCCACTGCCTAAATCCCTTGGTGCCCTCCCTAGGCTTCA GGGTAAGCCCTGACATCATGTGCTTTGTGATCTGTGTGACCTACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGTCTAAGGCGAGGAGCTACACTTGACTGCA
WI- 21028b	139 AG ---	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGACAAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTACAGGGG TTTC/AGJTGCACTGGTACAGAACACACAGGGAGTTTACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 AC ---	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGACAAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG/ACJATGTGACAG GGGTTTCACACTGGTACAGAACACACAGGGAGTTTACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 AG ---	---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG/AGJTTTCA TCATACAAGACAAGCACAAAAAGCACCACCCATGCCTCTGAGGAACATTTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 TA ---	---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGTT/AAATAACTTATGTGTACTTCTTGATTTC TCATACAAGACAAGCACAAAAAGCACCACCCATGCCTCTGAGGAACATTTGGACCATGCACCCCTTGAAA AA
WI-20964	87 GA ---	---	---	AGCCAACCTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGAAAT/AGACACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAATACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAAGAGGAAC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 TA ---	---	---	CTCTGAACCTAAAGGGCGGTGAAAGGCATGATTGGTTTGGCACACAGAGTGGATAACCAT/AAACAT TGGCTGGAATGAGGTGGTCAGGAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCTTAGGT
WI- 22130b	165 CT ---	---	---	TGTTTTTGAAGGGCTGTAGCAGACTACATAATGAGCGGTGAAAGGGCTGCCCTTCCCTCTCTGACAC CAGCAAGGGGGAGGCCACCATCACCAGCCCTGCCCATCATGCATCCAAATGATTACTAGCAGTAGGAA GCCAACGGAAANAGGACCCCGCGGCTTGTCT/CTGTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTCTGTGATGGGAATGAC

WI-21661	117 GC ---				GCTTAGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTAAATAAATAA[G/C]TTTAGTCACAGTC ACACAAAACCTACCTCTAAGGAAAACCTGTCCAGTGAAGCCGTTAAATTTGTGCTTTACGCTATGAAG GA
WI-21980a	25 TC ---				TCAGTTAAACACATTATCAAGGAT/CJAGATTAAATTAATGTCAGGTGAGCATAAAAGGGAGATTAA TAAACCAGAAATGTGTTTCTGGGAACCAAGTTTCAMGTGACTCAGGATAAGTTTATTATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 AG ---				TGCTGTATTAAATGTGGTGTACATTATCCTATTTACAGATGGAACACAGAAAATACCAGCTTTTT AAA/GJTAGCAATATCTATTATAATAATATTGAATAACACCATAATAATATCACTAAGGA AGTAATCTAATTGTGTTGATTTTCAGAGGGAGAAAACATTACCTCTAGAGCTAGGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112 GA ---				TTGCTATAATTTCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA CAACAGATAACATACCTGACACGGTTTCAGGCATGAAGGATACAG[A/C]AGTTAATTAACATAAG GAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAACTCTGGGGCC AAAACCCACTGAACCTACCCACGCTGAAACACTGAAGGATACCTGGGTAAGGA
WI-21524b	97 CT ---				GCCGTGAGGGTAGCGTATAATGAAAAGGTGTAATGACGCTGATGACGACCTTCGGCTACACTTAT AATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTCTCTCTGCAAAATGGACTATTGCCC CAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGGGGTGC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35 AC ---				GCCGTGAGGGTAGCGTATAATGAAAAGGTGTAATGACGCTGATGACGACCTTCGGCTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTCTCTCTGCAAAATGGACTATTGCCC CAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGGGGTGC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 GT ---				TTACCTTCCAAACAGGCCACCTTTGGAGAAAG[G/T]AAGAGATGCTATTATCAATAAGCCAGAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACCATCATCTCTGCCACAGAACC TTTGACATGCTGCOCTCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTT CTTAGGG
WI-21703d	197 AG ---				CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGTGGTGGTCTGGGAGGGGCTC TGCATCCCCTTTCTCAGCACAGCACCATCTCACCCCTCTCGGAAAGCAGCATTGGAGCCTACACCA CTTGCTTTTCTCACCCAGGGTAAGAAATGCAGGTTATTCAGAGGGGAGTGAGTCTGGGAA[A/G]G TGGGACAGACACAGCTAGGGGCAAGGACTTAAGGGAACCTGTGGGGGAAGAG

WI- 21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTCTGGGCGGGCTC TGCATCCCTTTCTCAGCAGCAGCACCATCTTACCCCTCCTGGGAAAGCAGCATTGGAGCCTACACQ A/GCTTGTGCTTTTCTACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAG TGGGAGAGCAGCAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGAAGAG
WI- 22683c	139 G A ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACCTGCGAGGTGAGCCGGCGCTCGCTAATCTTATTC CCAGTCTGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTTACAG GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGTAATCCGTGTGAATGTGGGT
WI- 22683b	55 C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACCTGCGAGGTGAGCCGGCGCTCGCTAATCTTAA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGTAATCCGTGTGAATGTGGGT
WI- 22683a	38 C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACCTGCGAGGTGAGCCGGCGCTCGCTAATCTTAA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGTAATCCGTGTGAATGTGGGT
WI- 22681a	52 T C ---	---	TCCTTTATCCTGCTGCTGCCTGAGTATTCTGGGAATCCTACAAGGATTGAGGAGCCCTTGGGATT CCAACCTAACAAATTAGTTTCTGTAATAATTA/GJTCTAGTCCATTAGATTGTGTAATGATCTAA ATGGNGTAACCATTTAATAATAAAGATAACAGCAATTAAGTCAGCTTTTCGAAGAAACTTTTATT AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCCTGGCTCAGTCTGAT/CJAGCACCAATTT CAAGTTTATGGCAAGGTATTTAACTCTCAGGCTCATTTCTCTTTGIAAAATTTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAATCAACTGAAATTTT
WI-20258	157 G T ---	---	AATCCACACTTTCACGAGGGGACCAAGCTGCCATGTCTGCCAGGCTCACAGCAGCGCGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGCGCATTTGGAACCGTAAGGCATGACAACG GGAGCCCGCGGGTGTTCAG/GTCCGTTGACGAGGTGCTGGCTGGCAGCGGCGCTCTACAGA AGGAGGAGCGCAATTCACAGCCCTTGTACGTAGTTTCCGGGGAAGTAOC
WI-22714	212 C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAATAACATTTTACATTTGTAGAGAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTCACACTCTCCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAGT CTGAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAGGATGAGGTGAGCTT ACCAACCCCA/CATGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI- 22734a	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGGCTG/ATCTTAGAAGACATTACCCA AATGATGAGAGGCAGCCAGTCGTCGAAGCCATAGTTGGATGGGAGACTTTTCCGGCAGAGGAAAT AGCAAGTGCMAAGGGCCTGAGGGAGAAATGAACCTTGGGCTTGTCTACAGGGGTGAAGCGCGCGGCT NTGGCTGAGGTTTAGTGGATG

WI-22724	117 A G ---	---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAGAGTGTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAACGTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAAT
WI-22750	48 G A ---	---	---	TGTAACCTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAATG[A/G]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAGGAGAGTCAGCATTTGACCATTCTGACTGTGCT
WI-22775a	60 A G ---	---	---	TGCTGTTCTTTAGTTTCATGACGTTTATCACAAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGGAAAATAAATCCCTAAGGGCAGCAATAATTTCTGCTTTTGAATCCTTCATTACAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGCTGAGGTATGTAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22808	143 C T ---	---	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAGAGAGTAGGTATAAGAACCCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A ---	---	---	TCCTCGTGTCTGAGCCCTCATCCCAACCCCTCCAAAGCCCTATGCCACACACACCCGTGTCACCATT CCCCATCCTCCCTGCTGCTCCCATCTCAAGTCCAAATTCOAAGCCAGAGCCCTGCCAGCTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGAGAGATGGGTGGAGCCAGTGGCTGTGGGTC CT[G/A]TTGGCGTGGTGAATGTGGGGGCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31 C T ---	---	---	TTGAACACCTGACCTGACCTCTGACATGGG[C/T]CTCTGGTCCCATTTGCTCCAACGGTGGCACA TCCTCATCTTTGTTATATACTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAAACACACACA
WI-21314	122 A T ---	---	---	CCATATCCAGTCTCTTTGAAGCTTCTATTGACTTTGGGTTGAGTTATTATCCTTTATCACTAT GACTTTCATTGATTTTATTTATTTGTTTCTCCATTTCTCTGCAACCTTTC[A/T]TTTGTATATAA ACTGTTTCTAAACTTCACCTTAATCTCTATCTGTATTTCCTGAGTTCCTGAACCTCTTTAGAGG
WI-21186	95 G A ---	---	---	AGCGAGCATCAGAAATCACCCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTGGAAGACCTTCTTAAGTGTGCAG ATGCTGTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTTAA GGAGAGACAGGAATCCAGAGAACTGCTAATTAAGCATAATGTATTGAAT
WI-21187a	94 A G ---	---	---	CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAATCAAAATACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GGNCTCAGTAATGCTCTAGTCCAGGGTCTCAA AGTATGGCTTCAGACAAGCCCCATTGTCATCACCTAGGGGAATGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAGCAACCTGT

WI-21190	39 T C ---				TTTTCCCATACCAATGCACCTGTTTGATATAAACTATTCGTTGGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATATTATAACAAATAATTAATAATCTGTACTATTACTGCG TTAGTTTCTAGTGTATTGAGAAAGGAGAAGTCAGCATAGTTATTTTCCATGTAAATAAAAGCTT AACACA
WI-19937d	186 G A ---				ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTCTCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCTTGCCTCAGGAAGAA
WI-19937c	185 C T ---				ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTCTCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCTTGCCTCAGGAAGAA
WI-21117b	227 C T ---				GAAACGGGGTGCTAAACAAGAAAGTCTCAGATCCCACTGAAAATCTGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAATACATCTGCGG TCCAATCACATCTCAGGTTCCAGCTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANITAGCAGT CCTCTCATTTCTACAGTCTGATTTTCCTTACTGAACTTGGGTGGGAG
WI-21122a	42 C T ---				TCACCTTTGATCATAATCCCTGTAAAGCTAAAGTTATTCA[C/T]TTAAGAGAACTCTGTTTTCC TTATTCAAATGTACAAGCCTGACGGTTACTGTACATATTGCTAGCAGGAGACAACTGGAATACT AAACAAATCTGGAAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTGTGGGTGCT
WI-21254	53 A G ---				CAGTTTGGTACAGGAAGGGCCCATGAATGTGGCGGGAACATTCACAGGAG[A/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---				AAGGAAACTGCATGGGTACAAAT[G/T]TCCAAATTCATCTTAACAAGGTGGGAAACGGGTCATTCT TGGCCTGCTCCAGAACAAAGGGCGGAGTCTATGCACCTCTG
WI-21059b	181 T C ---				GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTCAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTGATTTAGCCAGGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGTGACTATCCTTGCCTAAT
WI-21059a	63 C T ---				GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTCAGCTG AAAAATCCTGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGTGACTATCCTTGCCTAAT

WI-20442	37 T C ---				TCCACGTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAAGGTGGCACAATTTTAAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43 T C ---				GTGACAAGAGGTGAAGCAAGGGACAAAGGGCAGCAGGCGAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---				ATCAGAACTGCAATCTGCACATGAAAGACCTGGGGGAATGCCTACATCTGGAATT/CJCATTA ATCAACGTTAAATTTGTCCGACAGTCTTTCATTGCTGATCATTGATAATGACAGATCCAAAT GAACTCCTGAAGCAAAATGAATTTACCTTGTGCTTTCATGCAAAATTTAGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACACAGATCTAAGGAATTTGACAGGGATCTTCT
WI-21149a	167 G A ---				AGGACCTGCTCTCACAGTCCCTCAACCCACCCAGCTTTTGGCAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTATTTTAAACATGACCTTATTTATCTTTAACTTAACTGAGTCTTATATA CAGACCTGCCAACTGGAAGCTTTTACAC/GATGCTTCAGAAATGCGGCAGTATTGCACAATGGTT TGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-21376b	188 A G ---				GGTGCAACTTGGAAATAATGGTTTAAACACAGGATAAGCATTAAAGGAAAAACACITTTCAATGTGTC TTCCATTGATGAATTTTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAACCA GACAGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/A/GJGAAGTGATTCT GAAGTGAACGACGCTCATGCTGCTGCAATGGGAACTCTGGGGAAGAGCCT
WI-21382d	125 C G ---				CCATTGCAGTCCAGAGATGAGAACTGGACAGAGGCAATCATGAACAGCGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAGTGGGGCGGTTTGATCCAGTGGGATNTGGCTTCCC/CJGAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCAGTCTGATGGGGAGCAGAAAGCTGCCATCCTC AGTCAGGTCGAGTCCAGGGTCCGAGGAGCTGCTGCTCCATAGTCTCGCAC
WI-21437a	201 G A ---				TCCCTGAGGTGGAGTCCCTAGCATAGCTCCCTCCCTCAAGAGGGCAAGGGGTCAAGGGCAGAGC AAAAATCCAGTCTGCTTCAACACGGAGACTGCCCTTGGGATGGAAAGTTTCTGGAGCTCCCTCCATT CTATTCTGTGGGCAAGGAACATGCCAGGGCTGCTGTTAAATGGCAGGGGTACCTTTACCAGGGC/G /A/CAGGCATAGTGTGGCCCTGCTGCTGCTGGGGCCACCCCTGGGAACAGT
WI-21202b	156 A C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAATGGTCACAATAATTTTTAAAGTTAACTGATTATTGAGGG AGGAGGAGAGAGTTGACCAAA/CJGCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATGA TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATAATTTTTAAAGTTAACTGATTATTGA GGGAGGAGGAGAGAGTTGACCAAGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---				GCATGAAAAGAACTCCAATCAGACTTTTATCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAAGTG TATGATCAGCTCAGCTTCCAGTATCAACTGAGTACCTCATATGGAATTAATGCTAGGAATGACAA CAGTAAGGGCATTGGCAA/GJTCCAAAGTCATCTAATATAAACCATATTTTACATAATTTGTAGG GACAGTATACTAATCTCTACAATAATAAGGGTTTAAAATGIGTGTCTTA
WI-21627a	106 A G ---				GCATGAAAAGAACTCCAATCAGACTTTTATCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAAGTG TATGATCAGCTCAGCTTCCAGTATCAACTGAGTACCTC/GJTTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATAAACCATATTTTACATAATTTGTAGG GACAGTATACTAATCTCTACAATAATAAGGGTTTAAAATGIGTGTCTTA
WI-21399a	75 C T ---				GGATTTGAGTCCCACTTGATCTCAAAATTCACCTTCTTGCAATGTAACAAGCTCATTCCTCTAAAGTT TCAGTTT/CJTTTACCAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCCTCTGCAATTTGCTCTGAGGTTGTGTGTCCTAGGACTAGGTAGGATCTCTCTTGCTTTCTGCC TTACCTAGGCATAGTGCTGATAGCAGGCTGAAGCCCAATTCATCTGT
WI-2032ca	68 G A ---				CGATGCTGCTAAGATAGGAGGTTAATCTTTTACATGGTGGTGCACAGACAAGACATCAAT C/GA/JTCTGTAGCAGCGAGAGACACTTTAAGTTGCCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTCTGGCTTCTTAAACAGATAAACCAATCAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACANTGTGGCCAGAGATACCAGAGCCCTTGAGGGAAAGGCCCTCACT
WI-21249	155 T C ---				TTCTGGCATTCAAAATGTACATGTAAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAAATCACAATGTATCTAAGTTTCACTTTTAAAGAACATTATAAGGTAATT AAACTCTAGGTGTACTTAT/CJATGGAACAGTTTATTTCCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGCCAAATTTTCAGCTGTTTAAAGGAATTATAAACATTGAGA
WI-21504	147 C T ---				TGACACAGCATCAATTTTCATGAATACTTTGAAAGGGCCATTAGAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGGCACGGGCCGTTGGCTCCAGCTGGGTTTCCOC AGATGCAACAAT/CJGGGTTCTGGCTTCTCCACTGGTGGGATGGGATCGGCCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---				CTGCACCAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCCCTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAACCGGGCAGGGAGGGGAGAGAAAC/GA/CAC TAGCTTGGGGGTG GGCACCGCTTCAGACCCCTT
WI-21475c	181 A G ---				TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCAGTTGCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGACGTGGCTCTTTGGAGAAGGCA/GJ/AAAAGCCACAGCAGCAAC ACTAGGAGCAAGACCCCTCCCGTTCTCCACCCTATTTCCCTCCCTGAAG



WI-21475b	117 A T ---				TAGCCCTTCTGCCAATCTGGCAATNTGAGGCTGGGTGGACGTTGCCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCATCTTCTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGACGTGGCTCTTGGAGAGGCAAAAGCCACAGCAGCAAG ACTAGGAGCAAGACCTTCCCGTTCCACCCCTATTTCCCTCCCTGAAG
WI-20893d	207 A G ---				TGTTTGTGTTCCAGCACATCTTCTCCAAAGGAACCAACCCAGCCGTTGCGAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTGTCTACTGAGGAATACAAATCATTTGTACGTAAGTTATCACCACCTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTCAGJACATAACATTGGTAGAGTAAACAAACCAACCCACAGCCTAAATG
WI-20893c	179 T C ---				TGTTTGTGTTCCAGCACATCTTCTCCAAAGGAACCAACCCAGCCGTTGCGAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTGTCTACTGAGGAATACAAATCATTTGTACGTAAGTTATCACCACCTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACAAACCAACCCACAGCCTAAATG
WI-18941c	71 C G ---				GAGCTCAAGGAAGACCTTACCCAGATAGGACTAATCTGGAGGGTGGAGGAACAAAGGTGAAA GGTATC/GGGTCTGGTGAGACAAAGCAGGGGGCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCACAGAGGTGAGGAAGGAGATGGGGACATTTCCATTTCCAGTGCATGTCCTTAAAT AAACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAGCAAGACGCG
WI-21552b	166 C A ---				TGGGTACATGGACAGATGTATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCTTACCTCAAGCATTTATCCATAGTTACAAAGAA TCCAAGTATCTCTTGATTTTAAATGTA/C/AJAATTAAATTTATTGAATTTAGTTACCCCC ATTGTCTATCAAAATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21552a	66 G A ---				TGGGTACATGGACAGATGTATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCTTACCTCAAGCATTTATCCATAGTTACAAAG AATCCAAGTATCTCTTGATTTTAAATGTAACAATTAATTTATTGAATTTAGTTACCCCA TTGTGCTATCAAAATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21512	54 C G ---				TCCTCGTACTTCATGCTCCCTCCCTGCCAGAACCTTACAAAATAATTTCTGT/C/GJTAGAGAGGA AAGAGCTGGTCCCTGCTCTGGAGGCAACGTCCAGGTCGGGAAAGCCACTCGTGTGTGATCTGTC TCAGTGTGGAGGTCTCCACTCGCCCCACAGGAGCCCTCGGGGCCAGAGATGAGAAATGCTGTAA TCCAGTACAGGGGCTGCTGCTGGGGTCCCAACAGCTCTCTTTGGGG
WI-21513b	192 G A ---				CACATAGTTTCTCAAGAGAGGATGAACCTGAAACCTCCTTAAGGAGGACAAAGCACTTTCCATT ATTCTTAGTTTAGACCAGAACTTTAATTTTATATTCCTTTAAATTAACGTCAAAATACACCAATA CTTAGAGGAAATAATTCACAGTATACCAAAACATTTTAAGATAAAGAGGAGGTAA/GAJAGTAG TATCTCTACATACCACAGTATACAAATGATGCCTTCTCTGCAGGTTTAGGAAC

WI-21514b	133	CT	---			TTGAACCTCTGAAGGTGGCTTATGTCCTGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAGGAGCACATTACCATGGAGC[C /TACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCTTATGCAGGAATAAATGAGG ANITTAAGGCTCAGATGGGTGAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-21514a	100	AG	---			TTGAACCTCTGAAGGTGGCTTATGTCCTGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCA[AG/CTTCAAGGAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCTTATGCAGGAATAAATGAGG ANITTAAGGCTCAGATGGGTGAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27	CG	---			ATGAACATGTTGCAAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCAITCTACCTGTATGAGGGTACTT
WI-19576a	113	AG	---			TTGATCGGTTCTTAATACAGTACAATCCTTTTGTGAAACAAAGTCACACTGGCAATGATTATTACA GATCCAAATAGACTCAGGCTTCAGACATAAAATAATTAACATT[C/G]TCTAGTTCAGTGATTAGT CACAGAAATTAACAATCTGCCAGATGTACAAATTTGGTAAATAACTACAGCTTCTCTCCACGGGGA G
WI-21695a	141	AC	---			ATACACAGGCCACAATTGCAGGATGGAAGGCGAGTGGGCACCTTGGAAAGTGACTACACATGGCAATA AGCAGCCTATCTTTTACCACCAAGAGTTCTTGGGGCATGTGATGGCAGACACCCCTTTCCAA GGGAATA[AC/CT]ACTACACTAAGCCTACACTGTACTGTGAGAGTCATGGTGGAAACAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTGTTTCCAGANTTCTAAGGCCACAGCAT
WI-21574a	235	CT	---			AAACCAGAAATTTAGGTACTTTGTATTATGAGGAACCTACTATACTAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTCCACTGATCCTGGAGGTGACAGCTCAGTGAACAGGCG TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCTCAGAGTCACTAGGGAGCCATT GGCAGGCCAGGGAACCTTACTGCCTACTTCTT[C/T]GTCTGTCAGGTGGGA
WI-21644c	151	TA	---			TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTTAACCTTTCAGGAAGTCTTTGGGT GTGACCCACTGCATAAATGGATTTTCACCATANTATTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGAT[AT/CT]CAATCAAGATCCATGGAAATGATGCAGTTTAAACATGTGTTCTCAGC TTGCCTACTGACCACCTTTCCTTTCTAAATATGGCAACAGCACAGCAAGTC
WI-21614b	55	GA	---			TGCTTTAACCTCAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTAT[C/G]TTTTAACA AACCTCATTATGATCACTGTGCAATTCAGTCACCTAAATACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAAACCATCGTGTATTTCTAAGGTACTAGGGAGTT GGAACAGTACTACGGGTCAATGGTATTTTGGCAGTTGGCTGTGTGGG
WI-21615b	151	CT	---			GACCGAGAAAAAAGTGAAGGCATATGATGTTTGTGCAAGTATCAGTACTATTTCAAGCTTATAGA GAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACATATTAAGATAAGGATGGACT CTTCACTGAGTATTAT[C/T]AGGACACAAATCGACGGATGAATCTATTTGANTATACCATAGGCC TATCTATATTGGCCCAAGGGAAGGTAGGATGGGTACTGTGGAACCGGA

WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAATTAAGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAAATGCATGATGGGATAGACACTGTCTCTACAGATCCGTCTTTGGGAATTACAGGAACATAAAAGGATATAATGATGGGTTATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGGTTAAATTTGG
WI-21660	120 C T ---	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGGTGAACAGCCTCTCCACTGCTTACTGTGTACCAAGAGGAGCAAGCAGCTCACCCAAAGCCTAACCTGGCCCTGTGTCTTTTTCAGGCTTCTCAGGATGCCACAGCACATACTGGGAACTGGGATGAGGAGAACCCAGGGTCTGTCTTCAGGAGGTCACAGC
WI-19105c	211 C T ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATAATTTGTGGTCCATGTGGTTGAGTCTGTAAAGAAGGACACTAAGGCACATGGCTGGTGAATCTTTCGTATAGACACGGGTGAGCTCATGGTGAACCTCCTTGTCTGTAGGTTTCCAGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCAGTGGATCTCCCCACAACTTCCTCTCCAGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCC
WI-19105a	33 T C ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATAATTTGTGGTCCATGTGGTTGAGTCTGTAAAGAAGGACACTAAGGCACATGGCTGGTGAATCTTTCGTATAGACACGGGTGAGCTCATGGTGAACCTCCTCTGTCTGTAGGTTTCCAGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCAGTGGATCTCCACAACTTCTCTCCAGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCC
WI-21760c	81 C A ---	---	CAACCTAGTCACTCACTACTGATGCAAAATGATTTGGAGGTGCTTCTCTAGCTTTACAATAAGNAGGAGACCTCTGACTGCACTCACTCTCTCTGCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAACCTAGTCACTCACTACTGATGCAAAATGATTTGGAGGTGCTTCTCTAGCTTTACAATAAGNAGGAGGACCTCTGACTGCACTCACTCTCTCTGCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATAATTGTTCCAGCACCCTACTTACTGTTATTTCTCTTTGAGGAAACCAGGNATTAAAGAAATCTGGTTTGAATTTCCATGATGCCTAATCTATGTTAAATCTTTTCCCTTACCAAAAAGGAACCTTCTTAATCACCAGAGAAACAGAGGGGAGACTGAGATATGTTGCAGAAATTTATCTCTACCTCTAGAGACAATTCATAGTTTCAATACTTTTCAGGGTGTGCTTACTTGGGGGC
WI-20934a	72 T G ---	---	CCAAACATGCAACATAGTCTTCTTCTTAAAGTACATAGTAAGGTATGAAAAACATTTGTATTCAAGAAATTTGTTAAGACAAATGGTCAAAATATTCAATGGCCTGGCACTAGTGGTAATTCAGCAGACAAACAGCATGAGAAAAAGCGGGAGACAGTAATAATACGTGCCCATTTGCAATGAGTTACCCCAATCAAGCCCTTTTACCTCTTAAGATGGCAGATTAGAAAGACCCCTNTTCCCCAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATTCAGCCGGCCATCAGAACAAATAGCATCTATACCTTCGAAACCTTGTCTCTTAACCTCTCCAGGCAAGAAAGGAAAGTGCATATATGAATTCCTCAGAAATGGTGGGATCTCAAGACTTTTAGAAAGTGCTTATTAAGTATAGAGGCTTGAATATATATGATGATAAATGGTAGCCCTTCTGGAATAATAATTTTGTGTAATCTGTTTAAAAAGATTTTGTGATGCATTTGTCCTCCCA



WI-22082b	67 C T ---	---	CAGGACTTGTTGCTGCCAACTGCACATAAATGTCCCTTTTGTGTTGAGTTATGGTTGTGTCG /TGTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTGCTTTATCCGGATGACGG AGGGTACACGGGGCTCGCTCAGTCCCGCCGAAGGAGTATTCGCTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-20993	139 A G ---	---	AACACAACTCCATGCTTTCAAGATTCCACACCCAGATACTAAGACATATTAATAATTTACAGCAAT TAAACAGTGTAGTTTGGTACAATAACACATATAGCATATGACAAATTAGGGGAAAAAACCCCTGG GCTCTTAVGTAAACAAGTGAGTATACATTAAAGACAGTATGACAGATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTTCAGGCTCTTCCTAGCTCATCCACACATCACC
WI-21723b	125 A G ---	---	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAAATAATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGTTAGTCATATCCCCAAGJCAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82 G A ---	---	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAAATAATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGTTAGTCATATCCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99 T G ---	---	CAACAGATGCTTGAGCCAAAAAGCAAAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCCTTAATCTGACTTGCTTTACTATCTTTT/GJCCCCATTTCTCTAATCTCTTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCTATAGGAATGCCTTCTAGTTTAAATGTCCTGCCCCCAACA ATACTAACCCATTGAAGGATAACTATGGAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ---	---	TGACAGATCACACCACATTTGTTGTAACCTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACACATGTGCACACACIAGAGAGGCAAGTACAAAAATGTAACC CCACCAAAGTGCATGTGAATGAAAGTGCAAAAGGGCTTCATTGTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138 C G ---	---	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCCTGGCTTGGAAATAACTGAAAAAGATTGAT TTTCCTTTGTGTACAAAGGATTCAAAAATTTTCACATCTCTCTGCCAGTTAACGTGCCGTGG CTC/GCAATACACACCAAAGCCAGCGTAACTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166 G A ---	---	AATGAAAATGCCACCCAGAGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTGATTCCTCCATGAATTAAGCTGTGTGTGCTCACTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG/GAATTTACAAACCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGCAAT

WI-21079a	50 GA ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG/AJCGCAAAATCAAGT TGTTTAAATACCAGTGTGCAGCTTTGATTCCTCCATGAATTAAGCTGTGTGCTCACTTGTTTACA TAACTCAGGCCACCCCTGAAATATCTGCTAGTGGGAAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45 TG ---	---	TCGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAGT/GJTTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGCAATAGTCTAACAGTTAACATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAATATAAATAATTTGGTTGCAAAATCCAGNAAAGGGCA TTAACCAACATGGGACTGATCTCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79 AG ---	---	TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAAAGGACTCGGAAGATGTTGATCCAGGGCAGAGT GAGGGCAGACIAGJGGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGAGGCTCACCCAGAGAGCTCACTGCATTTGAOCCOCACACCCACCCTCACCC CAGCACACAGGCACACGAGGGGCACGACACAGNTGCACCTCACCAOCC
WI-18916b	42 CT ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC/CJTGCTTCCCACITCTTGGTACCC GGTTAACTGCCAGGNGGGTGACAGTGTGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCAOC AATGCCACCTTCATA
WI-18916a	35 GC ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGC/CJTGCTCAGCCGGCTTCCCACITCTTGGTACCC GGTTAACTGCCAGGNGGGTGACAGTGTGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI-19828c	200 AG ---	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAAGCTTTTAACTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTTGCTAAGTGTGTAGCCTAGTCCAGGNCCTTCTGCCCCCAATTTCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTTCTCTGACCCCTCACCCACCACCCAAAATJAG JCTTTTAACTCTGGAAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 CT ---	---	CACAAGAGTCTGTAAACCTTAGGGACACAGCCCTGGCCCTGCCCCT/CJTAGCTGCATGCCACCCCTC ATATCCCAACCCCATCCOAGCCTCTGCCCCCGACACCCCAAGGCTCCCTGCTCTGGTTGAAGTATTTT CTCAAGGCAGGAATGAGTCCTTGATCCAAACACAGCATCT
WI-19860	51 CG ---	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG/CJGJCTGCATCAGTAT CTCCATCCACATAATTTCTGTTTGTATTTTGGCATTCACCCATAAAATGGTGGATCTACCTCCCT CCTTGCAATTTGAGCTGNNCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19869b	80 CT ---	---	ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACCTGCAGGGCAAG AGGAGTGAGGGG/CJTAGAGCATTTATTTCCCTCTTTCACCTCCCTGTTAGCTTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCCTTGCCCCACAGTCGTAACTATTGC

WI-19891c	172 C G ---				TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATGCTTGGTGCCCTCCCCCCCCCG ACTCCTCTGTCTGGAAACGTGGCTTGNCTCCACACACAGTGTAGATGACAGCTCTCCTCAAGCGG AGCTCCGATCCCTCAATTTGCCATCTGTCTGACTCQ/GJCGTCTCCCGGGCGTGGGGCGTGTCTGT CAGCGAGCGGGCGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---				GCACCTGTAGGGGTAGCTTCCATGGTTCTCCAGCACCGGCTGTACATTACCTTAGGCTGACCAAT TCCCTTGGGGGGC/TJGCAAACTGCTTTGAGGAAATNTCCACAGGAGGAATAAACTAGAAAGCGC ACCTGCTATTTACCATACTATGGAGAAATACAGCTAATGAAGTGTGGCAGAAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTGTCTCCAGTCCAGAGAGACTTCTC
WI-20270b	91 T G ---				AGCCATACAATGCATTGCAAAAGAAACAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCAT/GJACACCAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTGTTTCCCGCAGAGGGCTGGGAGGCGGNGGGTGGTGGGA
WI-20270a	53 G A ---				AGCCATACAATGCATTGCAAAAGAAACAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACCAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTGTTTCCCGCAGAGGGCTGGGAGGCGGNGGGTGGTGGGA
WI-20622	130 T C ---				CCACTTTCATATTTTACAAATGCTCAGCGAGCAATATGAAAAGCTTCAACACTTTCCTTTGTGA ACTTGTGCAATAAATGCAACTTTAACAACATACAAATTTCTCTGTATCTTAAAGTTGAAT/GJ TACTAATTTTATGATGTTACTCATATTTTATTCATATACITTTAATGACATCATTGCCCAATACATA CATATTTCTNTAAGTTATTTTACAATAAGCCAACTCTGTCATGCAG
WI-20768b	190 C T ---				TTCCCACTCAAACTCCACCCCAACCTTCTGGAAGGCGAGGCTAACAGGACCTCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCCAGCTGCAATGCAAACTGAAACTCATCTGTATATCACCACTCTA CAGGAGAGGTCTATTTCTGGGGCACCCAGAGNTCAGCACACATACTGCTGGGA/CJTCAGGGGACTC GTAATTCGCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
WI-20768a	71 C T ---				TTCCCACTCAAACTCCACCCCAACCTTCTGGAAGGCGAGGCTAACAGGACCTCTGCCTGCCTGC TCA/CJTGACTGATTACTTTCAATCCCAGCTGCAATGCAAACTGAAACTCATCTGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGGCACCCAGAGNTCAGCACACATACTGCTGGGACCAAGGACTC GTAATTCGCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
WI-21909	153 A T ---				TGTTTGGCTTTGGCCAGGTACTCTACTGCTTTACATAAAATATCTCATCTGTCAATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAATAAGGATATTTGTTGGTCACTCTTTAAAGAAA TGTCCTTAACATACCAAG/ATJAGTGGAATCAATAGAATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACTAAATTTATATTTCTATGTATGGAAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTGCTTTCTGGAACATATTGGAACACTTGTTTTTCATAAGCTGTCCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTAATAAGGTCATTATGAATCTGAATTTCTTA/GJTAAAT ACTCTGGTGCAATTCATTTCATCTGCAAAAGCAACTGGCACAACCACTCTGCGGTGACAGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTCGCGGAACCTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAAGGATGAAATTTCCACATTTATTTTNCITTTATGTGAATAGAAATGGCAGTGAAGTGCCTATG AACTGAGGCGAGGAATGGCATGGCGCTGCGGTACAGCCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGAGGATCATAGAAAAAAACCCCTCAGCCAGAGTAGGACATTGTGATTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCGCAGGCTCTGGTTGT/CJTTCATTTGCAAAATAAAACCCA GACCGGTCTATCTTCAGTTCCCTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGATGATTTATCATGCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GAGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTTATGGGCTCTAAGCACOG GCCAGTAGTGGGAATGCCACATGCAATGGGTAGTGGGATCTGGGGGGGTGAGGACCTGCTTTT IC/JTCCAACTCTCTCTTAGCCAGAACTTTGCGAGAGCCCTTTNATTTCTCTCCCTCTATTCC CCCTCTTCCCAAATGTCTAAGTCCCAATCCAGACCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCTTGTCTCAGTACCAGAG/GJGTTTGAGTAC GGTCGTTTAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGGTCCATCTCTGGTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGCAACCAAAATGGCAGCTGGGCTAAGGCATTTAAACAAAGGCTCCAAAGGACCCCTT TCACTGGGTCTAGCATCCAGCTCTCTCTCAGCAAGGCAAGGATTGGTTC/JCCTTGTTTCTG AACAGGGCCCGAGGCGCAAGGCATGCCATCACTGACGCACTCAACCCCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAAATTTGTGTTTAAATTTCTATACAGAAATGGTCTTTCTTGAATATTTT GTAGGGATGGATGAATTGAAAGTGAAATTAAGTCAAGATAAAGGGGCAACTCTTTAATJAGJAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCCTCACCCAGCTACACTTTACCTTGTATCTATAAAGTGAATTTAGAGT AAATACATTTGGCTGTAAGTCGJVCJGATCAGGTGCTCTCCACCACAAAGCAAAACAAACTGCTGA AATGTGGCAAGGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGGNTCGCTTCCAGGCAGACGCCAGTGCCT /CCTGGATGGCATCAGCACAGGCTCCCTGCCCCGGCTTGAAGCATGGCTGTGTGCAACGAT
WI-21342d	59 T C ---	---	---	ATTTTCCCTTTCTGTGTTTCGTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGAAT/CJTGGA ATCTGCATGATTAAATAACATTAAAGTTTCATAAACACACCCCATATCAGAGTATAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATTCACATTCTCCTCCTAGTT T



WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCCCACATTGATCTTAGTTAACAGTCTTGTTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGACCCACAGATACTTCCAAGTGGAGCCAGCCCTCAGACTGTTCTCAGTCACT GCTCTCCACACAGCTGATT[A/G]CAGACATTGCCTGTGCTTCTACCCCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCCCACATTGATCTTAGTTAACAGTCTTGTTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGACCCACAGATACTTCCAAGTGGAGCCAGCCCTCAGACTGTTCTCAGTCACT T/C]GCTCTCCACACAGCTGATTACAGACATTGCCTGTGCTTCTACCCACAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCCAGTCGAGGGTGCACTTCTCCTTTATCTTGCTTAAGCCACTTGGGT[A/C] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTCAAGATCCCTGGAGGGAGGAGGCTTCTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGGGCATATGATTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCCTTT[C/G]GAAAAAATACACAATGGGAACGTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACCAGAGGCTTTATTTCAGCCACTCAGGACCCCTGGCTTCTGCTCCAAGGCACCTGAACA CAGTCAGGCTCTCTAAACACTGGCAGGACCTCCCCACAGCC[AG/CC]CCACAGGGTCTCTCTGTT TCCCAAGCTCTGATGGATTCAGGCAAGACCTTCACACATTACCCCACTACCTGCTGGAGAGGAGGGTC ATGAGGCAGCCTGTGGTGGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAAOCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAAGTCTCATGGACTTCTTCTTAAG[C/G]TGTCTATGATCAGAC CACTCTCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATAGGAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAAATTTCAACAATTTGACTATACAGAG TCTTCAATTTCCAAAACAGTTAATAGTAACTTGGTGGCACATACAACATGCAATTTGAATAGTCTGTAT TATTCACTAACTAAAT[C/JAGGNTCCCTGCATCACTCTCTCACA
WI-22250b	132 C T ---	---	ACTTGTCTTCAGGAGGCACTTCTGGGATCTAACTAGAAATCCTTGAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGAGTGGTTATTATGGGGTCTCTGCCCTCCTGGCTGTGTATG[C/T] GGANCCAGGAGTGGAGGAGCCCGTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGTCTTCAGGAGGCACTTCTGGGATCTAACTAGAAATCCTTGAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCT[G/A]TAGTGGTTATTATGGGGTCTCTGCCCTCCTGGCTGTGTATG GGANCCAGGAGTGGAGGAGCCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCCTCTCTCCAAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCOCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCCGCTGGCCCGAGTTCTGGCTCTCAGGACGTCOCAGCAAGTGA GCOCCAGAGGTTTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCCGCCAGAACCTG[C/G]AGTGTCTTC TTTGACGGGCGCGCGTCTCAGCTGCTCCTGGGAGGTGAGGAAGGAGGT

UTR- 04932-2a	149 C T ---	GCAGCCATCTCCTCTCAACACCTCCAGGCCACCTGGGGCCAGAGCAOCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCGCTGGCCCGAGTTCTGGCTCTAGAGTCCCGAGAGTGA GCCAGAGGTTTC/TJTTGGGACTCCAGCCAGGGGATGAGGCCAGGCCAGAACCTGGAGTCTTC TTTGAOCCGGCCGCGCTCAGTCTCAGTCTCTGGAGGTGAGGAAGGAGGT
stFIBBb	412 G C ---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACCTTCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCATGGTT
stFIBBa	341 T C ---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACCTTCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCCCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCATGGTT
stGLV2	61 T C ---	GTCACAAGGACGCGCTCGGGACGCTCCACCATGGCTGGGCTCTGCTCCTCAC/TCTCTC CTCACTCAGGACACAGGTGAOCCCTCCAGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGCTC TCCTGCTCCTCAGGCTCACCGGGGCCAGCACTGACTGCGCATGT
stSG1001 7c	70 T C ---	GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTCTGGGAT TA/TCTJAGGCATGAGCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1001 7a	33 G A ---	GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGCGTCAATCTCCACCTCGACCTCCAGGGTCTGG GATTATAGGCATGAGCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1002 3	63 A T ---	TAATGATAATTAGGCACTTCTCCACACGAAGATGACACAATTGACCCCAATATCATTTGAGGC(AT) AACAGTTTGGGCTGTTTTCCAGTAGTATGACATGA
stSG1009 6	36 G C ---	GTGGAGAAAGATCGTCTTCTCCTCCCTCCCATGACG/CCTGGCTTCCCGGGGACCTGTGCGTTTCC ACCCGAGACGGCCTTTGTAGGGAACCACTGCCACTCCGCTGCTGTGGCTTCCGCTCTCTAG GGCTCGAGTGTTAAG
stSG1011 8	107 C A ---	TAGGCTTAAAGCTGGAATCTACAGCCAAAGTCCCTCCTGCCTGAGGGAGTACCTCCATTTGGGC ACAGTCCAGACCCAAAGTCAAAGATGCCCATTTCTTGGG(C/A)CTCAGCCCTCAGTTCCTTCATTTC ACCAGGCCGTGCTGTTTGTAGTTTTCTCCCGAGTGA
stSG1012 0	89 T C ---	TAGTAGGTAAAGAAAGCAAGGAGGATTGCTTATCGCATGACTGTTTACAGTGGTGTCAAGACTATGC CGTGTTCAGCAACACTTTAATA/TCTGTGTTGTGTAATCTGATTTATCTCTGCTTACAAATG
stSG1017 8	42 C T ---	TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAGTCCG(C/T)GGGAGGAGAGTGAACAGGAA TCGATTCTTTGTCTTTAACTGCCCTAGTTAGGAGATGTTAAATACTTGGC

stSG1019 3	136 GA ---	---	GGACAATACTACCTAAGGACAAATACTATTATTAAAAAAGTCTTCTAGTGTATATTGGTAA CACATTTCTGGAGCTGGTAGGAATAACCATTTTATTATTTTCTGTAGTGCCATCTATACAAAACITTTTAC T[G/A]TTTGAAAACCTGAGATTTAAGTTGCAAACCT
stSG1020 2c	143 GT ---	---	AAGCTAACTTAGGTGAATGGTCCACTCAAAGGCTCTCCGAGGGAAGCTCAGTCTCGGCTTGGCAG AGTCAGCCCTGGTCACCTCATACGGGGCTCCAAGCTAAGCGTCAAGGAGCAGTCCCACCTGCTTCT CGCTGCA[G/T]CAAGACCACAAGGCAGAIGCCCACTGCTGCTCTTCTTGCTGCTAGCTTTCT
stSG1020 9b	75 AG ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCAAATAACTAATCTCCCTTAAGATCCCACTTTAT TTTTTA[G/G]CTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 CT ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATT[C/T]AAATAAACTAATTTCTCCTTAAGATCCCACT TTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 TC ---	---	TACTAGACATGCAAAATGAGAAGATTACAT[C/G]TGAATATTTAAAGAAGTTATATTTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAGTTAAAGCCAGTTATCTGA
stSG1025 2	108 AC ---	---	ATAGGTTTCAGGAACAAATCAATTAATGGAAAAATGAGAAGATCTTTATTTTGGACCAATTTT AGGCACTTAAGAGTTTCTTTCTCTCTTCCCTTCCCTTGATCA[A/C]AGTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTCTTG
EST10915 0	123 AC ---	---	CTGTATTAAATGAAGGGCACTATTAATGAGGGACGGAAAAATCTACCTGTACACAAAATTTCTGTAC TTTAACAGCATCTTCAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG[A/C]ATTTTAA GAACTGAGTTATTGGAC
EST11023 1	166 TA ---	---	TTTTTTGTTAAACCAACCCCTGAAAGTTCCACATGTGAAATATAGATACAACAGTGAACAAAAT ATGTGGCCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAACAGCAGGGC AATTAGTCAATTAATAAAAAATAGTACATGTTA[T/A]GTGTAATAAAATTAATTTACAAAAGGCTTT TCCACTCGTGGATTGATTCCTTTTTTGGAGGAGGGAGTAATCCTGG
EST14096 8	71 GC ---	---	GGGATGTATATTACAGATAACACAACCTCACAATAATACCATCAGACATTTGAAAACCTAAGGCCATTCT GTGA[G/C]TTATTTTAAACCTGGTGTTTGCACATAATGATCTTAAAAAATAATGAATTACCAAA ACCAAGATTCTCTTCTAAATGAAAAATTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 CA ---	---	TGCAAAATTGTGAGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTAGAATGTGAGGTGG CAGGGATGCTTAAGTCTTCCTCTGGCAGAGACCCGAGGTGCAGAGATGATTCTTCTCA[A/C]A[CCCTTTC TCTCAGGGTCTGTTGGAG
EST22555 7	60 GA ---	---	TCAAGCATGTGTAAGGCACCTGCCCGCCGACACCCCTCTAACTTCTGCACACTGGAAGGT[G/A]AAA CCTGGAGAGAGAGAAGACACTCCCTCCCTAGCTTCTAOCCTGGGCAACCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ---	---	GTAAACCTTGCAACGCGCATGCTAAATGGAAGCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC[CTTGACATGGGCCAAAAGACTTCCAGACAAAGCACGGGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGAACCTTAACCTCAGGCTGCTCTACTCA[ GTTGGTTGCTAGCCTCACTCGCACACAGGAAGCTTGGAAITTTGAGGCTCCAAAGTCACTCTCCA GAGGGGGAACCTCAAGAGGATCCACAGTGAAGCAGATCATGGGCAAAAGTC[AG]CTATGG GGCCAGACTGAGGTTGGACACACAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCGCG ACAGCAGGAGTAGCCAT
EST36745 3	56 A G ---	---	TGTGACCATACCAACCTATGCAATAAAAGAAAAAATAATCCTCACCTTAAAAAACAACAAAA AACCTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGG ATTTATGTTTGAATAAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGTATG T[AT]TATGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410c	201 A T ---	---	TGTGACCATACCAACCTATGCAATAAAAGAAAAAATAATCCTCACCTTAAAAAACAACAAAA AACCTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGG ATTTATG[GT]TTTGAATAAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	TGTGACCATACCAACCTATGCAATAAAAGAAAAAATAATCCTCA[CT]TTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTT GGAATTTATGGTTTGAATAAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	TATCGTGGGAAGTTCCAACTCATACTTATGCTGCTTTTCTACTTGTCTAATATTGGATGCTTCTTGCCA GGCTC[CT]TTAAATTGCTGTAACTGGGAAGAAACCTTCTACTCTCCACAAACCTTGAA
STS- R42778	74 C T ---	---	CAATCTGAAGAGATGCATAGCGGATGGTGGCTTTCAGCAGCTGTTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCCCTCCGGGATGGTGAATAATGTTCCGGACCTAGATA[CT]GTACCGA AGGTAGCAGCAGACTGTGAGTGCACATA
UTR- 04350	125 C G ---	---	GAAATAAACTAAACTGCAAGCAAACTACTGTTAATAAGAAATTGTTCTTCTGTTT[CT]GACAGTTG AAGTGGGTGTGAGATGGGATAGCAATGAACAGTGGGAGCCATGAGGCTCAGAAATGCGGGCAAA CTCCTCTGTGAAATGTAT
siSG1026 6	55 T C ---	---	GTATAATTCAGCATAAGCCAAAGCCCTTTTAAATAACCAATACTATCATTTTATGAATCTTTTACA AGA[TT]G[AAGCAGCAGTAGTACAATAATTTAAGCATCTCAAGTCTCCAATTTAAGAGTTGACTATC
siSG1028 2	70 T G ---	---	CACITTAGATATGAGGAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTTCATACCACGTTGAAACCATGTGTTTATATGCAATAAACAGCAATAATTTTTCACCTC[AT]TTG TCAATGCCAATGCATTGAAGGCCAGAAAATGAGAAAAGGATAACAAACCTTTTGATAAAAAAGGTA AGAATTTCTGTGTG
siSG1031 0	128 C A ---	---	

stSG1033	116 T C ---			TTTAAAGCTACATGCTGAAGAAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCCGG GCTCAACCTGTCTAGGAAGGCTAGACCTCAACACCAACACCTCCATTC/GCATTTCCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCCCTCCAGCTCTCTGGGCTGCTTCCACCTGTTTCATCTGA CTTAGACCCCTCC
1b				
stSG1033	107 A T ---			TTTAAAGCTACATGCTGAAGAAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCCGG GCTCAACCTGTCTAGGAAGGCTAGACCTCAACACCAACCAATTCACCTCCATGCATTTCCCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCCCTCCAGCTCTCTGGGCTGCTTCCACCTGTTTCATCTGA CTTAGACCCCTCC
1a				
stSG1243	225 GA ---			ATTGGCAATGGGAAATGACACCAATCAATTTGATTACAGAAAATGGTTTTATAAATCCCTCCTCTTG AAATTATGTTCCAGGCCAGCATGGTAGCTTATGCCTGCAATCCACGACATTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTGACACCAAGCTGGGCAACATAGTAAGACCCATCTCTGTTTTT TTTAAAAAAGAAATTCGTTC(G/A)AAAGTATTTACAGACCAAAAGGAGGT
b				
stSG1345	60 GA ---			AACAGCTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACCTAGTTTGCTTCTTAC(G/A)CGCT TCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
b				
stSG1345	54 T G ---			AACAGCTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACCTAGTTTGCTTCTTACGGCT TCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
a				
stSG1385	117 T G ---			TTAATGTCATCCAGGAGGGGCCAGGATGGAGGGGAGGGTTGAGAGCGAGAGCGAGTATTTT TGGTGGGATTCACACATTTTCCCATGAAGAGGGGAGACTTGGTATTTTG/GTCAATCAATTAAGAA GACAAAGGGTTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTGCTCG
b				
stSG139	69 T C ---			TCGCTCCTTCCAGTCTTCCAGAGCATCCCATGATGTTGACCGCACAGCACATTTGTGCTCT TT/GCTTTAGCAGCATTCGCACCTCTGGCTGGTCTGCTGCCACTGATTGTACTGCTGCTGCTGCC
				GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCAGTGGTCAAGGCTCTGTTGTTGTCATCCCT TGCTCCTCCACTCCAGTTTGGCTTCTGCTCCTC/GCTGCTCTCTCCATGTGGCAACAAAGATGGC TACTGGTGGTCCAGGTTACGTCCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGTTCTACTCCCA AAGTCCATAACTCAATCCCTTGGGAAG
stSG1427	103 T C ---			CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTTAGTCC/GCTCCCTTGCATGA AATGTGGGAGAGGGAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---			CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGTTC/TTTAAATTCAAAGGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAATGCTTCTTCTTAGTCTGCAGATGGGTA
stSG1483	44 T C ---			CACACCCACAAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCAAGTGTGCA TC/GAATGTGGAGGATGCTGTTGCAGCTGTAGTTACTAATGCAGGAAAAACCCCAATGCAAGAGGAA AATGCCTGA
stSG1696	67 C G ---			

siSG1847 b	95 GA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACG[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAATTAATAAATGATGACTGTGCT TCAACACAACCTG
siSG1847 a	49 CA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAANTGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAATTAATAAATGATGACTGTGCTG TTCAACACAACCTG
siSG1897 a	83 AG ---	---	CTTAATGCCCTTCTCTCTCTCTGACAGGAGACAGATGGGTAACATAGAGGATGGGAAGTGG AGGAGGACACAGGACTT[G/G]GCCACCACTTCTCTCTCCGGTCTCCCAAGATGACT
siSG2022 a	86 TC ---	---	TGCTTTGAGGTTTCAAACTCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATACAT[C/A]TTCCATAATCTCATCTATTAAACATTAAACACAGGCCCTTTGTGT TGTTATTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCTCAGTTGGGGGTTGAC T
siSG2076	104 CG ---	---	AAACGTTGTCCCAAAATTTGTTTCAGTTTCAAAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAAATATATTTTGACATT[C/G]ACATCAGAGTGGGGCATTTT
siSG2108 c	71 AG ---	---	TTGAGCAACAATGATTCCGCAATTTGGCAGCTCCAAACCAAAATGATTGAGGGGCTCCACAGAGA GAGC[AG/TA]AGGGGAAGACTTTTATAGGACAACCTGTAGAAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTTGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
siSG2108 a	49 TC ---	---	TTGAGCAACAATGATTCCGCAATTTGGCAGCTCCAAACCAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAAGGGAAGACTTTTATAGGACAACCTGTAGAAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTTGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
siSG2141 b	173 AG ---	---	TTATTCAGGGGACAAAGCTGCACAAAGGAATGTTCTCTATTTATTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCACTGGCAGTGGCGATGGTCAGGTTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[AG/AA]AGTTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATCTCTGTTGCTCTG
siSG2141 a	113 CT ---	---	TTATTCAGGGGACAAAGCTGCACAAAGGAATGTTCTCTATTTATTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCACTGGCAGTGGCGATGGTCAGGTTG GGTCAGATTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATCTCTGTTGCTCTG

stSG2148	50	A G ---	---	TGGAAACAACCGGCTATAGTCTAGTCTAGTCTATATTTTAGACCGTGATTC[G/AAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGATTTTCGATACTTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68	C T ---	---	CTCAATGAGGACTCCATCAGCCAMCGGTTTATATGGCAGATGAGCTGTACAAATCTGTTGTGCT [C/T]GCCGCTGACTCAGCTAATGCTACCGGGTTGAGCGCACACCGAGCCCGCACCTTTTCCAT ACCTGGGCAGAGGGAGGGAGTGAAGGAACA
stSG2189	41	C T ---	---	CAAGTGTGAAAGCTGGGATTTGAGCCGTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACCTCATCGTAACTTTGAGCACCTAGTGTCTGAGTACTTCGTATAGGTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49	T C ---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGCTGTTCTGTATGATG[T/C]TTTATATTTATGAT AATGCTTACCTGATGATACCCCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85	G T ---	---	CATTTCTGCCCTCCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G/T]AGAGCATCTCCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
stSG2257	65	A C ---	---	TCAGTGATTGAGGAGCTGGCTAAGTCATGCTAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[A/ C]CTGTCAGGAACTCTGCCAAGCACTGGCTGCTCCTCAGCAGAATTTCTCCT
stSG2306	67	A G ---	---	GTCAACGCGTAGAGGTCACCTGGTATAAACAAACAGTAGCTATATGATAATTTGGGAATAATTTTACA [A/G]TATGCTCCCATTTGGGTTTTCCAAACTGATACACCATGAGGTGAACACATTTTCACTGTTTCACAG TTCTCCAGAGA
stSG2334	70	T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCGCAAAAAACA AAAAAT[G/T]GCACTGGAGGGGCTGTGGGAGGGTGAATG
stSG2339	63	T C ---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAAATTGCTTGAAGTGCAGAGTAAGTGTGCTAC[T/C] GTTCTCAGAGTCACCATTAACGGTGAAGTGTCTATTTCTGGCTGTGCTTCTCTATTCATCA
stSG2465	76	C T ---	---	CAAGCTAAGAAGCCGACCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCACCTCAAAATG CAGAAACA[C/T]TACAGATTAAAGAGAAACACACACACACATTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGGGGTATGCA
stSG2549	140	T C ---	---	TTGCAGGCTTGTATTCACAAATAACAAGTCATGTATAGAGAATGTGAATGATACTTGAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTTGTAGTACTGGGTTAAATATGCAAGCAGCTAAAG GAATAT[T/C]TACACCACCCACCCCTTTTAACT
stSG2577	123	T G ---	---	AATTGCCAAATGAAATTTCCAGAGGATTTTAGACCACTTTGCCCTGTGCTATCCAGTTTGGT CCCAATATAGGCTTCTGCAAGAGAGATCAATGCCGAACCGAAGTGTGAAAGCAT/G]GAACAATC CCGGCCCAAGATTAAITAT
b				

siSG2577 a	121	CT ---	---	---	AATTGCCAAATGAAATCCAGAGGATTTTAGACCAACTTGGCCCTGTGCAATCCAGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAAGTGTGAAG[C/T]ATGAACAATC CCGGCCAGATTAATATT
siSG2700	58	GA ---	---	---	ATCTCTGACTGCTTTAGTGGGAAAGGAATCAATTTATTTATGAAGTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTGGGGAATAAACCACTGGTCCAGAGCAGAGGAAGGCTACTTTGAGCCGGACACCA
siSG2724 b	101	TG ---	---	---	AAACAAGCTTTGTCAATTTCCACTACATTTGTTGTGCTTTATATTAATTTGCAAAATGCTATAAT TTAATACTTATATCCAAATGCTTGCATAATCAAT[G/T]TTTTTAACTCTGGGGTGTGAAGAAC
siSG2776 a	65	GA ---	---	---	GTGGCCGATCTTTACTTTCCAGAAAGGGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATGGCCCTTTGGAGTTAGGCCAGGAACCTTCAACAAGGGACACTGCTGGCCAAACCAAAAA ATATCCACTAATCCGAATATAGTAACCCCTGTCTGTCCGAATG
siSG2791 b	109	GT ---	---	---	AAGGAAAGGTGGAGGGAAGAGGGAAGATTACAATGGTTAGAAAGAGCAACTAAAGATTATTTC TATTATCTTCTGAACGGTAAACTAGCAATTTTAATAATATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
siSG2791 a	100	AG ---	---	---	AAGGAAAGGTGGAGGGAAGAGGGAAGATTACAATGGTTAGAAAGAGCAACTAAAGATTATTTC TATTATCTTCTGAACGGTAAACTAGCAATTTTA/G]TAAATATTTGGGTCCACTTAAATCTATTA AAGCAGAAAGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
siSG2826	85	CT ---	---	---	CCGCAATTTCAACACACATTTCTATGAAACTAAGGTGGATCATGTACAAACACAAAAAACAAAGC TCCCTCCCTCCAAAAACAAA[C/T]GAACAAAAATAAGAAAGAAACCCATGNAATGCCCAGGTTTA ATTTTTTTCC
siSG2850	88	GA ---	---	---	ATGGGTGCATTGTAAGGCAATTAATACTTTTTCAGGCAGGGCTGGCAAAATTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCCCAT
siSG3031	71	TC ---	---	---	ATACTCACGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCCCTGGCATTCTCTGGTGTGAGC AAAT[C/G]GCCCTTTATTTAAATGATCCAGACATCTGGGCAGCATAGCT
siSG3058	81	GA ---	---	---	GTCCCAACTCTCTCTCTTAGAGAAAAAAGTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAGTCAAAAC[G/A]TGAAAGAGCATCAAGCCAAAAAGGCAAACTGGCTGAGGC
siSG3092	94	TG ---	---	---	CAGCATCTCCAGAACATTCCTAGAACTGAACCATCTCTGTCACTATTGAAAAACAAAGCCAAAGTTC CAAATCCAAATAATAATGAACGTGC[T/G]GATAAACATTTCTTTATGGTTCCAGCCCCCTACTTT AGTT
siSG3230	95	AG ---	---	---	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATGTGAGTGAGTC[A/G]GTGGGTGCTAAGTGTCTGAAGTGAAGTAG
siSG3245	160	GC ---	---	---	ACATCTATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTGAGAGGCCAGTGGGGTGGCCACTTGGTGTCTACACCCCTGCTCCATCCAGTCTG GCCCAGTACCTACCTGGGAGGTT[G/C]TGTACTTGGCTTAAGTACTTCATGCTTTAT



sISG3285	42 T C ---			AGGTAAATGAGTACTAAATGTAGCATTTATTTATAAGGAATGCGCATTGTGAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTCAGCCACATTCAGTGATGTTTCTAAATACACAAATCGAC AGGACTGCTGTTCAAGTACAAATGAGGACAGCTTTTCAGGCAATGGGATTTCTTGATAATGCTAA ATCTGCTTGTGAGCTGAATTTCTTGGGCTTATGTGGCAGTGTGGTAAAAA
sISG3269 b	141 C T ---			TGTAATCTGCTGTCATCCTATCCCTCCCTGAGCTGGACTGCTCTCCAAAGGAGACTAGG AGTGAAGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGAC/TTGTAGATCCCAAGTCCCTGACACATTTTCTTAAGAAACT
sISG3269 a	24 A G ---			TGTAATCTGCTGTCATCCTATCC/TAGTTCCCTCCCTGAGCTGGACTGCTCTCCAAAGGAGACT AGGAGTGAAGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTAAGAAACT
sISG3284	130 C T ---			TTAACTCAAGAACTTTCAGTTACAGGAAGATTTATCTAATATTAATGACTAAATTACAAAAGC ATAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCA/C/T/ TCCTAAC/TTGTAAATGCTGTAAATGGGACATTTGTTTGTATACCCC
sISG3292	99 A T ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTACTTAAATATCTAA/TATJACAAATCAATAGCATTTTCTAACTTCAA TAAATGTCATATCTTTAGCTCTCACT/C/AJCCAGTGTATCCATTTTCCCGAGCCGTAGAGCTTTCTG TTTCTGTAGATTTGCCTGCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTGACACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGATGCTGAGTCTTCTTCTTAA
sISG3369	69 C T ---			GATCCCGAGTATTATTTCTAAATGAACTTGTTGTGGAAATAAAAAATCTGAGGACCACCTCAGAG GG/C/TATAAGGGGAACCTCTTTGCTTGTAGTTCATAAGGACTTTCT
sISG3398	125 G T ---			CAAGACTGAAGAACGTAGGCTTTGTGAGAGTGAAGGAAGGATGCTCGAACTTCCCAGGACTCAGG CTTCAGCTTCACAAATCCCGAGGAAAGGAATGACATTTCCAACTGTCACTTTGTAGC/G/TJCTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
sISG3416 a	43 A G ---			TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCAGG/WGJCTCACTGTAGCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCTGCGAGGACAAAGTCACCATGCTTA CCTAAGTTTTGTAGAGACAG
sISG3424	173 T A ---			GTAAGACAAAGTTTGTATGTTGACCAGGCTGGTCTTGAACCTCTTGGCTTCAAGCGACCGTACCA CCTTGGCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCGCGGACTTTTAACTGAAT GTTGAAAATCATTTCTGCTTTTGTGGTAACTGAT/AJCAAGTTGCTTAACCTTTGTGAAACCCAC TTTCTTATCTGTAAACAAATGGACAACAGAACTTTTCTTCTCTCTC
sISG3436	88 T A ---			GTTTATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGTCAAGGTGATGGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGCCCC/T/AJGAAATAGCTTACTCTGTTTCTCCTATC

siSG3463	103	CT ---	---	GATACAGAAGATAGTGGTATGGATGGATAGTATGAAGGACAAAATAATACAAATATATTTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTGCAC[C/T]GGAAACAAACTTGCTTGACTATATTA CTGA
siSG3491 b	71	GA ---	---	CAAGATACTTCATTGTCTCTAAGTAGTGCAGTCTGGCAATAATTTCTCAGCAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCACCTGTGGATTCTATTAACTCATTATATACTATTTTCTGTGATG ACAGAAAATAAGTTAAC
siSG3523	33	CT ---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTTTC/TGCAATATATGTGTACAAACACACACACACACC CCTAATTCCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
siSG3536	213	A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAAACCAAAATACAGATGGCTTC TGTGATACTGGCCTTGTGAAACGCATCTCACTGTCAATCTATTGTTTATTTGTTAAATGAGCTTG TGCACCATTAG[G/T]CCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
siSG3583	112	GA ---	---	GAAAAAGCTTAACATACGATCCATGTGCAAAACCCAAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
siSG3586 a	60	GC ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACT/AAAAATTTAAAAATCAGGTGTGGTG[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
siSG3589	101	TC ---	---	ATATAGTGTGGTAGCATTTAACTCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAAGT GTATATACCACCCCTGGCACAAAAACCCCAATGAT[C/C]CTATTTCCAAAGATGTATCCAGATGAAA GTATCCAAACAACAAAAAGCTATATACAC
siSG3590 a	70	AT ---	---	GAGAGATGAGCTATTTATTTCTTTTAACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAA AA[A/T]TTCTCTGATGTCCTTGACCCCTGTAGGAACACATTCAGTTTCTACACT
siSG3619	78	AC ---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTTAGCAACAACTCCAGAGAAAACTGGGCTCTATATATTTAAG
siSG3644	40	TC ---	---	ACATATGTAACCTGCCATTAGTAGCCATATTTAGGATGAGAT[C/G]GGATTGAGAGGATGAACCAAGG ATGCGTAATAATCATTATGAATAATAAGTTATCTGGGGAACGCGCCATTTGTCCAACATTTACTAA GTGCGCTACTA
siSG3646 c	70	GA ---	---	CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATAATATGCTTACT GGT[G/A]ATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTTGAGAGTCATT CTTCTCTTTGTA

stSG3646	55 A G ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATAATATGATGATAACAATA[A/G]TATGTCCTT ACTGGTGATATTAACTTTGATACCTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646	43 A T ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATAATATG[A/T]TGATAACAATAATATGTCCTT ACTGGTGATATTAACTTTGATACCTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693	85 A C ---			ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAAACCCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGGAAAAAGG
stSG3693	30 C T ---			ATTGTTTCCCTGAACATTCCCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAAACCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGGAAAAAGG
stSG3698	145 G A ---			TCTTGCCCTTTGTACCCCTAGAGAGATGGCACCAATCCCAAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATAACCCACCTTCCCTCCTACTGCAGA
stSG3698	51 C G ---			TCTTGCCCTTTGTACCCCTAGAGAGATGGCACCAATCCCAAGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTA AGTCTTTATTGGGGAATAACCCACCTTCCCTCCTACTGCAGA
stSG3724	107 C T ---			ACCAGCCTCATGTGCAGAGGTTCTCCTGCTGGATCCCAACTGGAGCCATCCCTGGGCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---			GCCAAAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAAATATATTATTACCAGCCCAACAGCAAAACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128 G A ---			CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGTTTACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGAAAGAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
stSG3787	49 T A ---			TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTATTAJAAAGTTCCTAAGA CACTGAGGGCATAAACCAAAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGATATCTTCCCCT
stSG3880	115 G C ---			GACAAGAGGGGAAGAGATGCGCCAGAGACCAGGGCTGGGGCAGCTGGGGTCCCTGAGTGCCAGGGCGC CACCACACGTCTGTGGTCAAGGCCCTCTCTCTGGGAGCAGGTCTA[G/C]GGCAGGGAGGATGCAG GGCTGGAGGGGACCCCACTCGGGGACCCAAAGGAGTCCATTCTGCCCC

siSG3880 a	36	G C ---	---	---	GACAAAGAGGGAAGAGATGCGCCAGAGACCAGGGCTG[C]GGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGCTCTGTGGTCAAGGCCCTCTCTGGGAGCAGGTCTAGGCACGGAGGATGCAG GGCTGGAGGGGACCCCACTCGGGGACCCAAAGAGTCCATTCTGGCCCT
siSG3895	44	A G ---	---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTG[C]A/GJTTTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATTACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAT
siSG3902	104	T C ---	---	---	TCGTGTGAGACTGGAGAGACCAGGTACCAAGCACCGGCTCTGGTGGGAACCTCGCTTCCTGATAACA TCATCTATTTCACTAAATGTGAACCTGCTTTCTTTCT[C]C/CAGCTCAATAGCTTAACATCTAATTC ATGTTTGTCCCTTTGCTGGACAAT
siSG3935	50	G A ---	---	---	GGGTGTCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[G]A/CJTAGTGTGCAGGC TCCTCCCAAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGGACGT
siSG40	25	A G ---	---	---	GAGGAAGAGGTTGAAGAAGTGTGTA[G]AAATATATTTAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTAGAAATAGGAACAAATAAACCCCTTGTTATGTATCA CCCAA
siSG4009	32	A G ---	---	---	GTGTGGCTGTCTGATGATGAATGGCGGCTCJAGTACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCCACACTGCTTACA
siSG4033	123	T C ---	---	---	AGAAGCCTTGGGACAATGGCAGTGCCCTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAACACTACAGTGCAGTAACCAAGAACCCTAATGTTTTCAAGCATAAAGGTACTTT[C]JGTGAAC AGGTGGCAACAC
siSG4038 a	29	G A ---	---	---	GCTGAGACACGTGTACAGCCACGCCCTGT[G]A/JGCGAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGACCTGAGGGTTCCATCACT
siSG406	53	T C ---	---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAAT[C]JGGTTTTAGTT TTGCTGAAGACTGGCCCTTATTATGGACAGCTTCTTAACAAGAGATTATTAACTTTTATCAGGTGT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55	G T ---	---	---	ATCTGGGCTGAATTAGTCAAGCAGGTGATGATGCTGCTAGATGTTAGTGTATGTTATGTTATGTTA GTTTGTCTGTAACTATTTAAAGCTTGTCTATCTCATCTGTAACCTATGTGCTTGAAGATCAAG CCTTGGACTAACCCAGGGCAATGCCCTTCATCTGG
siSG4095 a	27	A C ---	---	---	ATCTGGGCTGAATTAGTCAAGCAGGT[C]A/C]GATACTATTGTCTGCTAGATGTTATGAGTAAAAA GTTTGTCTGTAACTATTTAAAGCTTGTCTATCTCATCTGTAACCTATGTGCTTGAAGATCAAG CCTTGGACTAACCCAGGGCAATGCCCTTCATCTGG
siSG4120	65	G A ---	---	---	TGCATGTTCCACATCTTTTCAACAAGCAAAATGTATAATAAATTACGTACTTATGGATAATCAC[G] A/CTTTTCCCTCAGAGAGCCACAGTTAAACAGTTCCAGCACACCATTAATCCACCCGAGCT

siSG4128	54 A G ---				CTTGGCAGATAAGGGACTCGTTGCAGATATGACTTTCCTTTGGTACATTCTT[AG]TATATTAATTT TACTTCTCTGAAATGCCACATAATTTGCAATAAATGATTCACTCCTTAGTCTCCAAAAGCAAGTCC TTTATCAAAATGCAATGTTCCAGAGGG
siSG4209 b	128 G A ---				CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCGCACTCCCTC[G/A]GC AGGGGACCACGGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
siSG4209 a	65 G A ---				CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG /A/CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCGCACTCCCTCGGC AGGGGACCACGGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
siSG4254 b	31 G A ---				CATTACCCAGAACGCCATGGAGGACAGAGC[G/A]CCACGGCCGGGACTCCCGGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCGGGGCTGCCTCTCCCGAGGGGAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCCGGTCATG
siSG4301	81 T G ---				TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAVAGAGGGGTAGTGGTCCCACACTTTCAT TTAAGCAATAAATTT/GJAGCTCTGAGTAGTGTGCCAGTTTACCCACATTTTG
siSG4331 b	71 T G ---				CTCACAAGGGCCCAACACAGAAAAGATACAAATACATTCATCCAGCTAATATTAGTTTTATGACAC AGAGTT/GTTTTCAAAACAAGTTTAAGTGTACCTGAAGAGCATGTTAAAAAGTTTAAAGTTATCATT GGAGAGCAGATTTCTTGGCCTCGCCCTTGTGATTTCTTTGAGGGGTGTC
siSG4340	76 G A ---				TTTTGCAACAACATGGATGGACCTGGAGGCCATTAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGAGATAAACAAATGTGTACACCTGGACGTGGAGAGCAGAA
siSG4361 b	109 A C ---				TTCCCAACCAATTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTTCTTGGAAATTTCCATAAGGGATAAATGTCATCTTTTGC/[A/C]CCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
siSG4361 a	24 T C ---				TTCCCAACCAATTGAGTGACAGAGC/[C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTTCTTGGAAATTTCCATAAGGGATAAATGTCATCTTTGCACCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
siSG4376	73 A G ---				TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTGCAAGTGGCTTCTCAAGGGGAG AACAG/[G]CTGGAACTGGGCTCTGCAAGAGGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
siSG4381	50 T C ---				GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTTT/[C]TCAGTCTTGTAGT ATCCACAGTAGTGCTGTCTCCATGTACAAGTGTCTGCCAGACACCCCAATTAATTCATGCC
siSG4410	79 A/G ---				ACCAATGGTTCTGCTATGTGCATCCGATAATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAAACACCGC/[G]TGACAACGAACCCAGTGGACTGTGAACCTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

siSG443	65	C T	---			AGCAGATCAGTCAGCCACTTGTCTCTCTCTCTTTAGGAGAGGCTAGGCAGTGAACACATCA/C/
siSG4430	54	A G	---			TJGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGAGGGAGGGAATAGGCAC
a						AAATGGAATCTATCTGCGTGTCTCTCTCAGGTC
siSG4448	99	G A	---			ATGCACATTAAATGAATGGCCTAACTACTGGGAATTTAGTAGTTCTATAAGGT/AGJATTAAACATA
						GGTAGGATCCAGTTCTCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGGCCATTTT
						CTCCCTCCCTCTCTCTCCCTCCAGTCTTTCCATACTGTCTCCCTCCCTCCCTCCCTCCCTCCCTCT
						CGCCTAGCCCTGCCCTCTGGGTCACCTGCG/ATJGGGTAGGCCCCCAAAAA
siSG4449	92	T C	---			ATTAGCCATTCTCTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
						TAACTTTGGACAACCTTAAACTTAT/CTJTAGTGACATTGCTGTCTAATAATCAAAATACITTCATCATA
						GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCC
						CAGACATGAGGGATGGCCTGTCTCTCTGGGACAGAGCCTCA/C/AGATGATGTCCATGTTTGTGT
siSG4467	42	C A	---			GAATGAAACTCAACACTCTTCAGTTTTTAGAGTCAATTTCTGGTATCGAGCGACACACCGAGGAG
						CACACCTGCTTCCAAAGGCTGCTGCCCTTCTGCACACAGT
siSG4475	21	A C	---			ACATGTCATTTCTTGACACAGG/AC/ATTAATAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA
						TTAAGAGACACAACACTGGACTTTTGTCTCTTTTCTTACTGTAGCACCCAGGTTTCATG
						GTAACATTCTGGGGTGGGGTGAGACAACAC/AGJATGAACCAATAATTAACTAATATACATT
siSG4477	32	A G	---			TCAAGGAGACTTTTAACTAGGTTAATGTGAACCGCAGCCATCAATGGTTTGTGAGGAAAAGGGAGA
						TGAAGTCTTGTCTGGGGCAAGCTTTGGCCTCATTTGCAGTCAGACTGGC
						TGACTCAGAGCTGGTGGGAGCTGCAGCAGGGGAGGCTGGGGCCGACAGATGAGCCGCCGGGGA
siSG4531	79	C T	---			CAGCAGGCGTGG/CTGCCACGCTCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTTGGACTCGATCT
siSG4550	86	G A	---			GAITCTCATTTGACAGGGGAGACGCTGTGTGTCATCAA
b						TGCATTAAAGGAATGATACGGCATAATTTGGGGGACAGAGAACAGGCTTGTATGAGGACAGAGTCTATTT
siSG4550	85	C G	---			AAAAGACAGTGGGCAC/CA/CAATTGGAGGGGAAGGGGGCAGGGTTTTAGAGAAC
a						TGCATTAAAGGAATGATACGGCATAATTTGGGGGACAGAGAACAGGCTTGTATGAGGACAGAGTCTATTT
						AAAAGAGACAGTGGGCAC/CA/CAATTGGAGGGGAAGGGGGCAGGGTTTTAGAGAAC
siSG4590	47	A G	---			AATCAGGCACAAGCTCGGGAGAGAAGCCAAACAAAGCTCTTCTGCAC/AGJATGGGAGGGAGACAC
						CATTGAAAAGGCATGTTCTCTTCTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
						AATCTGTATCACCCAGCGTGGT/CA/CAATGTACTAGTAGCTTTCACAGGGATTTTTTATACTATTC
siSG4623	22	T C	---			CTATAAGGTTTTATCATGAATAAAAAAGCTCAACAACCTTTTCAGCCATTGCAGATTTCACATTTATCT
						TAATATCTCTGTTCAAGATGCTCTGGAG
						TAAAAAAAACAACCCCCCAAAAAACACCCAGAAGTTTTTGTAGTTTTTATGTTTTTCAGATTTAAAG
siSG4843	102	A C	---			GTAATTTCTTTCTAGCTTCTAAATTTTGTAGTCA/CA/ATCAGAAAGTCTTCCCTACTCCCAAGGTGA
						GAAAGGA

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[illegible]

ESTD- AT3a	--	--	--	---	---	AGACCTCAGTTTCTCTCTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCCGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAGGTGGAGGAAATTTGAAAGGGCATTG GAATTCAGAGCAAAAGACAGATATTAAAGAGCTGGGGAATGTGG
ESTD- B3AR	--	--	--	---	---	GGCTGCCAGGGTTCCGTGGAGGCGCCCTAGCCCGGGCCCTGCTGGGCTGGGGTCTGGCCACC GTGGAGGCAACCTGCTGGTCACTGTGGCCATCGCCCGGACTCCGAGACTCCAGACCATGAACAGT GTTGTGACTTGGCTGGCGGAGCGGACCTGGTGTGGACTCTGTTGGTGGCCCGCGCGGCGCCACCTT GGGC
ESTD- BA511	--	--	--	---	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGGTAGCAAGTGC CTGTAGTCCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTGCCTGCA
ESTD- BCL2	--	--	--	---	---	AGCTGGATTAACTCTCTCTTCTCTGGGGCGCTGGGGTGGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTGCTTCTCTGGGAAGGATGGCGACGCTGGGAGAACAGGGTACGACAAACCCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGCTACGAGTGGGATCGCGGAGATGTGG GGCGCGCCCCCGGGGGCGGCGCCGCAACCGGGCATCTTCTCTCCCA
ESTD-BCR	--	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCGGAGACTCATCATCTGCGCAAGA GACCAAGAGGTCAGCTTCTGTTGCCCGGAAAGGAGGAGGAGGTGACAAGCTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCTGGCACA
ESTD- BRCA1a	--	--	--	---	---	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACCTGGTACCTGGTAC TGATTATGCCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	--	--	--	---	---	ACTAATGTAGAAAAATCTGCTAGAGGAAACCTTTGAGGAACATTCATGTCCACCTGAAAGAGAA ATGGGAAATGAGAACATTCAGATACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAATGTT TTTAAAGAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAATGACATTAAAGGAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGAGTCTAGCCCTTTCACCCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGGCCAAAGA AATTAGAGTCTCAGAAAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGATCCTCTCCCTAATTTGCTCCGGGAAGACATTTCATCAA CCCAGTCAGTTTGGGGGACAGCCATGCACATGAGCCCTCTGGTAGCCCTTCAACCATGCATTCCATCTAA GCTCTGCAAAAT
ESTD-C6	--	--	--	---	---	



[illegible]

ESTD-D7S399	--	--	--	--	--	TGAATCTTAATTGCTATCTCTACAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCTACATCATCTCTTACAAACATTTTCATCCTGACTCCATACCTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	--	--	--	GTGGGGACACGAGGGCTCCAGGCTGGGGCTTGACGTGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGGAGGGAGACA GAATGCTGATTATCTGGTGGAGAACAGAACTTCTGGCTGTGGGTAGGGGAGCTGCTTCCAAAGACC TCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DRD1	--	--	--	--	--	TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAACGGTCAGCACCCCACTGAACCTCGAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD-DRD2	--	--	--	--	--	TCTGCCTTTGGTCAGGAGGCTGCCCAGGAGCCCAAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCAGCCACCAAGCTGACTCTCCCGGACCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCCCGCAACCCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD3	--	--	--	--	--	AAGCAGTGGCCAGGATGAGCGCCAGTAGGAGAGGGATAGTAGGCATGTGGCGGGGCTGGCTGG CACCTGTGGAGTCTCTGCCACAGAGGTGATTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCCAGAGGAGGTGGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD-ERB82	--	--	--	--	--	TCCTTCAGGATCCGATCTGCGCCTGGTTGGGCATCGCTCCGCTAGGTGTCAGCGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTGAGTGCAGCGGGGGCGGTCCAGACCCACCGGGCTGGGAGGACTTCAOCC CGCCTCACCTCCGTTCTGCAAGCAGTCTCCGATCGTGTACT
ESTD-ETS2	--	--	--	--	--	ACTCACAGTGCCTTTAAGTGAATGGTCGAGAAAGAGGCAAGGAGGCCGCTCTGGCGCCTGGCA GTCCGTGGGACGGATGTTCTGGCTGTTGAGATTCTCAAGGAGCGAGCATGTCGTGGACACACAC AGACTATTTTAGATTCTTTTGCCTTTTGCAACCAGGAACAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGGTGGGAAGGAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F2	--	--	--	--	--	GATAAGTACACTGAGGCCCCAGGAGGTATTGCCTAGTAGOCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCCTCAAGGCCCGGTAGGGGAACCTGGGGGATCTAGGGGATGGGTAGGAATGGCC AGCCCAGTCCCGCGGTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	--	--	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTATGATTTATGCCCA TGCTCCATTTGAGTTAATTTTGTAAAGTATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGCCAATTTAACCAGCACAAATTTGTTAAACAAAAAAC

ESTD- GODH	--	--	--	---	---	CGCAGACCGGTGAGTGGGGTCGGAGGTGTGAGGGAAGGAGGAGGAACCTGGGGTTTAGGGACT TTCCGGGGTACTTTCCCGTTCTGTGCTTGCAGAGAAAGCGGGAGAACACAGAGCACTGGCTAA GTGTAAAGGGACCTCTGTGCGCACCGGTGTCTGCTGCCCTGTCAGCTGTCTGTGCTGCCGACGTGA CTCTGTCCCGGAATTCGAGAGCT
ESTD-GCK	--	--	--	---	---	GTTTATGTCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTGTCACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACACACCTGGCTGG AGCAGGAATGCCAGCGCGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCCAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	GACCCTGAGTAOCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCACAGGCATCATTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD- GPPK2L	--	--	--	---	---	AGTCTTCATCTCGGGTGTCCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	--	---	---	CTGGGCTCGCCCGCAGCAGCTGCTGGCACCTGGACGGCGGCCAGGCTCAOCTCTATAGTGGGTGG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	TTGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCTGGGCCACACTCTGGCCTTG AGGCCCTGCAGAGCCCAAGAAAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTACCAAAGCTATGATAACCTTAATTACACCCCTGAGCAAGAGTTCCGGCTCCGGCTTGATCC AGATGGAGCTTCCCTTATCCCTGATGATTGGATTGGCTTCCTGCTG
ESTD-HT2	--	--	--	---	---	GGGTAAAATTCGAGCAACTTTCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTGAGAGAGAATAAAAGGATAACCTGGGTTTCTGTGC TTTGCTTCTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	ACCAACGAGCCGCGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAAGTAGGTTCTTGGTGCTTCTATCGGCAAGAAATCGGTACTTATTTGAATAGTAGAGGTAA ACCACACGCCCAAGAGTCACTGAGACTGGCAGCTTCTGACGAGCGGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGGCGCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	AACACACAAGCCCGCAGCGAGAATTGAACCTCGGACCCCTGGTTTACAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTGCTGCTGTGGTTTCTTCTCTTCACTTATAGATTGATGTATGCTCTCTA GCATTCGGGCTACCGAATAGGATGTTAGCTTGAGTAAATCCAGGATTTCTCCTACAAAATGAAA ACATTTCTGTCTGTAAATCCCTCGAAAGTTCT
ESTD- IGFBP1	--	--	--	---	---	ACCCAGTGGAGCCGCTCATTCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAAGGAAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	--	---	---	TTTACTATTTCATGATACAGAAATGTGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCTACATTGTGTGAGTGACGGGAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTGAGAAAGCAATATGAAAGATGAGTATCTATGATACGAACATGAAAGT ATGTAATATCTTCAAAAATACTATAAACGGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	---	---	CAAAGTAAGACCCCAATAATGTAGCTATTACTATCATATTATTATTATTATTTATTTTGG AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGAGTGAGGCAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTCAATGCCATTCTCGCTCAGCTCCCGAGTAGCTGGGAATACAGGCAACCGGCACT GTTCCGGCTAATTTTGTATTTTGTAGTAGACGGAGTTCAACGT
ESTD-IL1B	--	--	--	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCTACCTTGGGTGCTCTCTGCTCAGGAGCTCTCTGCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATAT AAAGGAAGAAAAATGCATTTTAAAGTAAGTGTCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCTCACCCCTCCCTAGCCGTGGGAGCAGGAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCCCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCAGTCAACATTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTGAGGCTCAGTTAATATTCAAAATTTGAACGTAGCAAAATGCAATGGTATTTAGA AAAAATAAAATTTCCAATATGATGTGTGTTATACCTGCCTCTGCCATGCAGCATATAGCCTGT GGGAACCAAGGAGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTTCCTTACCCATTCACTGAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCCACTCTTCAGCTCTGGCTGTCCCTGCCTGCA AGGTTTTGCTTAATCTCAATCAATGCTCTTCATCTTTAGCAGCTGTGGGTTTTGTGTGTTTC TTCGTTTTGCTTAGTATCTGACTACTTTTTTAATATAAAGAGAGATGATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCAACAACATTTATAAAATTTTTCACCTG
ESTD-MOC	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCTCCCAAGCTCTGTCCCTAGCCGAACCTTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTGTCTTCCCAAGGTTTTGGTCTAAGTGTCTAAGTGTATACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGTTCTCTGTTTAGCATGG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAATATACCAGATCCCAAGACTGATATGGCTGGT

ESTD- NFKB1	--	--	--	---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAAGAAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCTAGCCCAAAACGCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGGAGAGAAAGATCATTTGAAATTTCTGAG AAACCTCTTTTAAACCTCACCTTTTGGGGGTTTGTGAGAAGGTTATCA
ESTD- NPPA	--	--	--	---	---	TGTCCCTAGGCCAGCCCTGCTTGTCCCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACAGAC AT
ESTD- NRAMP	--	--	--	---	---	GGAGGAGGAGGTGGGAGGGGCTGTCTGCTCCAGGTCOCACAGAACAGAGAGCGGCCCTCAGTG TATCCCCACCCCAATGTGGGCGCTGGAGATGAAGAGGAGTTGATGCAAGT
ESTD- NRAS	--	--	--	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTATGTAGGTGATATTGGATACCTTTTGTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTC ATCCCTGTGGTTTTTAATAAAAT
ESTD-OTC	--	--	--	---	---	GTGACCTTCTACCTTTAAAAAATTTACGGAGAGAAATTAATATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGGTATGTAAACA
ESTD-PAI1	--	--	--	---	---	GCCACCAACCCACCCAGCACACCTCCAACTCAGCCAGACAAGTTGTTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGTCTTGACACGTGGGAGTCAGCGTGTATCATCGGAGCGGGCGGGCAC ATGGAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTAGACAGACAAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	--	---	---	CTCTCAGGAACCAACAGCTCTTACCAAAACAGCACTTATGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTCACCTTCTGTGTTCTAGAAGCTTTTCTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCC
ESTD- PBDA	--	--	--	---	---	CCTTCTCATGCCAGATGAAATCCAGTCCCTCAGGATCTGCCAACCCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAATCTTACCCGACGCTTGTCTGCATACAGACG GACAGTGTGGTGGCAACATTGAAGCCCTCGTACC
ESTD-PS-1	--	--	--	---	---	GGGAGTAAACTTGGATTGGGAGATTTCTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGACACACCATAGCCTATTCTGTAGCCATATTAAATTTGTGGCTTACATT ATTACTCCTTGGCATTTCAGAAAGCAATGCCAGCTCTCCATCTCCATCACCCTTTGGGCTTGTTT CTACTTGGCACAGATTATCTTGA
ESTD- PXPPI	--	--	--	---	---	ATGAACATGGTCTTTAATTTTATGATATGTTTGTATTAGTATCTTAAAGGGCTTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGTGACAAAGGTGTTTTTCTCAAGGCTCATACAGA TTCTGAAAATCATGTGTCCTAGAACATTTTGTAAAGAGGTAGTCTTATGAAATTAATCTT
ESTD- Pai/RDS	--	--	--	---	---	ACCTACAGACGTGGTGGATGTGTGTCCAAACCCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGAAGAGCGTGGCGGAGACCTGGAAGGCCT



ESTD-PDS	--	--	--	---	---	---	CCCGAGGAATCTGAGCGGAGAGCGAGGGCTGGCTGCTGGAGAAAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAACAGGTGAAGCCGAGGGCGGAGACGCGAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGCAACACTGAGAAATAGTGCACT CCAGAAACGTGGATCTCCCTCATCAACTCCGAAGTCTGAA
ESTD- RYRI	--	--	--	---	---	---	CTTCGTGACGGGAGGTACAGTCTCCGCTCTTTATGGACATATGGATGAGTGTCTGACCAATTTCCC CTGCTGACAGTATGACAGCGCAGACTTGTCTACTATGAGAGGGGAGCTGTGTGCACTCATGCCCGC TCCCTGTGAGGGCTGGAGCCACTGAGAATCAGCTGGAGTGGAGGCCAOCCTGGCTGGGGCCAGCCACT CCGAGTCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGGAGG
ESTD- SPTB	--	--	--	---	---	---	TGAACACCCCTGTGGTCCGGAGCCAGGTGTGTTTCTCTGGGAGCCTGAGGAGTGTGTGTGTGTG CAGTCCCGCGCCACCTGCTGTTGAGCCTGGACATACACCTTCACTCTTGGCCCGGAGAAAGAC ATTTACACACCTGGCCATGTCCCTGGCCTGTTGTGCACACCTCTGTGAACCCCCAACCCCTGCCCTCC CCCCCCAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	---	TTCACTTTGTGGATTGTTCTTTGTGTGTCAGCACCTTTTCAACATGATGTATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGTGGGATATTTGAAGAGATCTTGGCAGTCCAATGTCTTAGAGAG TTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTAGATTAAAGTCTTTAATCCATTTTG ATTGATTCTGTGA
ESTD-TAT	--	--	--	---	---	---	AAATGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTCATCAGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTGTTTACACCTTTCTCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACACATCA
ESTD- THPB	--	--	--	---	---	---	TGGGCCCTTCTCCGGCAGGGTAGACTTCTTACTGGCTGTTGATTTCCAGAGAAAGAGTCCCAAG CACACGAACAGAGTTCAGATCCCATGAGGCCCAGTCTCAATCAGACAGGATCACTTCATCCA CACTGGATTGGCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	---	TTCTGCATCTGTCTGGAAGTTAGAAGGAACAGACCCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGAAGGGCATGAGGACGGGGTTGAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAGACCCCCCTCAGAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGTATGCTT GTGTGCCCCAACTTCCAAATCCCGCCCCCGGATGG
ESTD-TYR	--	--	--	---	---	---	TAGTGAAGTTTTCATCTCCTGTGAGTCTGGAATTTCTGTTCCCAACCAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTGTCTTCAATGGGCAAAATCAATGTCTCCAGATTTTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGATCCAGACAAAGAGTCAATAATATTGATGTGCGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

ESTD- TYRP1	--	--	--	---	---	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCACTTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATACTGTATTTCTTTTCACCTTATTACCTCTTCTTCT AATACAAGCATATGTTAGAAATTAAGTTCTAGGCATACTT
ESTD- VB12	--	--	--	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACAAAGGTACAGACAGAGCAAGAACCCAGTG ACTCTGAGATGTCACAGACTGAGAACCCCGTTATATGTAAGTATGATGATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	--	---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTTGG TCOCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCCTGCAGGATGTG CGACGTGCGCTGGAGTAGCCCGGACTCTTGTACGGTCGGCATCTGAGACAGTGAGAAAGGCCCTT CATGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	--	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGAAATTACTAAGGCAGGACACAGAGGCTTAATTGA TATCCCAAAGTTGAATGTCTCAGTTCGCTGTGGGTTAGATGCAGGATTTATATGATCCGTTAAC TCT
EST71770 6	--	--	--	---	---	AGCACCACTCTCAGGTCAGCCTCAGCACAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTTATCCTGAAGTCCGGATCTATGACTCAGGACAT ATAAATGTAAGTGTGATTGTGAACAACAAAGAGAAACCACTGACAGATACCAGCTGTTGGTGAAGG AGTGCCCAAGTCCAGGGTGACACTGGACAAAGAGAGGCCATCCAAAGG
EST52418 6	--	--	--	---	---	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCCAGTCACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAACACTGTGAGTGTGG
EST13586 3	--	--	--	---	---	CCCACTCTATTGCCAGCCCCAGGACAGAGCTGATCCTTGAACCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCAGCCAGCCAGACCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGCTGCTTAGAGACTGGAGAGGAGGTGCGTCTGCTGCCTGCGCCCG GTCACTC
EST51976 7	--	--	--	---	---	AGGCAGAACTGGGCCCCCATGCGGGGGACGTGGAGGCCACTTGAGCTTCTTGGAGAAAGACCTGA GGGACAAGGTCAACTCTTCTTACGACCTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGGAGCAGCAGGAGGAGGAGGATGCTGGGC CCTTTGGAGAGCTGAGCTGCCCCCTGGTGC

EST11458 6	--	--	--	---	---	CCACITTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAACAAACATTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	---	---	---	CGGTCTTCCTCCAGGTATTGTCAGAAGGCCGAGATGACCTCTATGTCAGATGCATTCATTAAG GCATTTCTGAGGTAGTACACCTTCCCACTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAGGCCGTGTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	---	---	---	ACCTGGTGTGCTGGTCTGTGGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCTCGGGCCCGTGG TCCTCCTGGTGGTGGTGTCTGTGGAGTCAACGGTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGAAACGATGGTCCCAAGGTCCGATGGTCAACCCGACACAAGGGAGAGCGGGTTACCCCTGG CAATAT
EST36027 2	--	--	---	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCCTTCATGGCCTGCTGGCCAACTATGCTCTCAGA ACATCACTACCCTGCAAGAACAGCATTTGCATACATGGATGAGGAGACTGGAAACCTGGAACAAAGG CTGTCACTTACAGGGCTCTAATGATGTTGAACTTGTGCTGAGGGCAACAGCAGGTTCACTTACACT GTCTTGTAGATGGTCTCTAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	---	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAAGTCAAGTGGTTTACTCCTCATGACCAAAATATCTTCCCTCTTAGGATGAGGTGA TAGTAAATGACCGATGGGGTCAAGACTGTTCTGTCAACCATGGAGGATATACTATACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 EST44438 7	--	--	---	---	---	ATGCTAAGGGGATCGGACATGAAGGACCCCTGTAGCCGATGTCCTATCTCCAGCGCCCTGTCTATC CAGTCACTCATCAATGGGCCAGTCAGGCCAGGCACCTGGGCTCCGAGGACTCAACCACTGCCCCCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG GCAGCCAGGAGCGCTGCACCATGCCCGCATAGATGGGAACCTCAAGCTCGACTTCAAGGAGCTCCT GCTCCGACCTAAGCGAGCAGCCTCAAGAGCCGAGCCGAGGTGGG
EST12839 3	--	--	---	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTGTCT CCTAACATCTATGTACTGGATTATCTAAATGAACACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGAAGTACTTGAAGTGAAGGAACTTGAATGTTATTTCAACTGG ATTTCCAGTAGGTTTCAAGTTACTTATGAATATTATGATACTTAGCTTAG
EST54419 8	--	--	---	---	---	CTTCTGCCTAATTTGAATGATATTGCTGTGGGACCTGAGCATTATGGCACAATGATCACTA TTTTCTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGTCTACTA TAGTCCAAGTGAA

EST10398 2	---	---	---	---	---	TGCTGGGTGGCAAGGCTGCAACAAGGAGCAACCCAGGAGGCTTTTATGAAGCGGGCATGGTA AGATGCTGCCACCTCTTATCTACTTATGATGATGTTACATTTGGGCTTGACCTTCCAAACACGGAGAAG CATTTGTTCTTCGGGCAAGAAGGTATCTACCATAGTGTCTATAGGCAITTG
EST36751 7	---	---	---	---	---	CCAACTCGTTCAATTTAGCTTTGCAGGTTTAACTCGATTACTTTTCTTATCAAACTCTCTGTAAAA TTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	---	---	---	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAGAATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTTCACCTGGATGCAATTAATAACAAATATTTACCTTTTGAAAAATAAATG AAGGATTTGACCTGCTTGGCTCTGGAAGAGATACCGTACCTGCTGACGTTTGTGAACAATACAGAT GCCTTCCCTGTAGCAGTTTTCAGCCTCTCTACCCCTA
EST18288 3	---	---	---	---	---	GCTCTATACCCCTGTGGTCTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTCAACACCTACGTCCACITTCGAAGGTAAAGGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	---	---	---	---	---	TTCCGCGCAGCCCCCATCTTGGCACCCCTGGTCCCTCAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCTCGGTAAACATCCGCGGGGCGGCTCTTGAGACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTGCCAGGGGCCAGCCTGCAGAGAGAGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
EST58707 7	---	---	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAATAACCTTAATCATCAATTGTTACAGGAGGCTTT AAGTTGAGCATCTTTGGCTCACATGAAGCCAAATTCGAGAGACCTAGAGATACAGAGACCGA ATGTATCAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGTGGTAGGCCAGTTTATAGCA CACTTGTACCTACATTTCTGATTGGTGGACTCTTGTGCTAAGAACCTT
EST74167 6	---	---	---	---	---	AGACCATGAAGGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACGACCCCGGTGGCGGAGG AGACGCGGGCACGGCTGTCAAGGAGCTGCAGCGCGGAGGCGGCGGCGGACATGGAGGA CGTGGCGGCGGCTGGTGCAGTACCGCGGAGGTGCAGGOCATGCTGGCCAGACACCGAGGAGC TGCGGGTGCGCTCGCTCCACCTCGCAAGCTGGGTAAGCGGCTCTC
EST43211 8	---	---	---	---	---	CGCCTGGTGCAGTACCGCGGCGAGGTGCAGGOCATGCTGGCCAGAGACCGAGAGCTGGGGTGGC CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCGGATGACCTGCAGAAAGCGCC TGGCAGTGTACAGGCGGCGGCGGCGAGGCGGCGGCTCAGCGCCATCGCGGAGCGGCTG GGGCGCTGGTGAACAGGCGGCTGGCGGCGGCGGCTG
EST36770 4	---	---	---	---	---	TGTAGCCAAAGTCACCTGCATCATTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACGGTTTCTGCTTCTTCTGATCAT TCTTACAAGTTATACITCTATTGGAAAGGCCCTAAAGAGGCTTATG



EST65258 8	--	--	---	---	---	TGCCCCATCAGCGGGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACAGAAAT CCAGTTATTTCCACCCTCAAATGACAGCCATGGCCGGGCTCTCTGGGGCTCGTGGGGGG ACAGCTCCACTCTGACTGGCACAGTCTTTCATGGAGACTTGAGGAGGGAGGGCTTGAGGTTGGTGAG GTTAGGTGGCTGTTTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	--	--	---	---	---	ATCAGGATGAAGGTGGACAGGAGGAGGGCCAACTGTCTATCCACAGGGCTGCAGATGTCGCTG GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 2	--	--	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCAATTTGTTTAGCATTAACCTAA TTTTTTTCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAAG TTTTTTTCTCGAAGTCCAGTATTCACAGAGTTTGGTTTTGAAGTACATGCCTGTGAAAAA GAAACTGAATACCTAAGATTCTGTCTGGGTTTTTGGTGATGCA
EST35879 9	--	--	---	---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGCGGTTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGACCCAGGCTGTACCAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCGAAGACAGCAGCGGGATGGGGCAGGAGAGCTGCCTGGATGAA
EST68308 5	--	--	---	---	---	GGAAGAGATTAAAGAGCTTGATTGGACAATCTGGTCTTTGAGTGTGGAAGAGTTTATGCTCTCT GCCTGAGTTACACAGAACTCTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA
EST54045 6	--	--	---	---	---	GGAATATTAAAAATTTTAAATACCTCCATTTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTCATGTGGCAATTTGTTTCTTACAAATCGGATGGGAATCT GTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAAATGTGACTTTATCAT
EST52908 0	--	--	---	---	---	ATCACAGTCTCTGGTCTCTGCCCATCTTCTCGGGAGAGATGGATGGTGTGCAAGCCCTTTGG CAATGTGAGATTGATG
EST19590 2	--	--	---	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAATGAC
EST76136 2	--	--	---	---	---	TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACCGCGTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0	--	--	---	---	---	CTCTGGATGGTTACAGGTGGCAGGCACAAGCCAGTCCATCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGAGAACAGGACAGCCACATGGCGGGATGGCCGGGGAGTTCTGGT TGCGGCACGGCTGTGGCTGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGTTCT TGCCCAAGGAGGGGGGGTGGCCATGCCTGAGATGTAGATGCGGGC
Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence						

- 305 -

## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that  
5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the  
10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

-306-

## CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.



-307-

12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which  
10 is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining  
comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.

-308-

20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method  
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.